

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2003, 05:13:50 ; Search time 3743 Seconds  
(without alignments)  
18002.148 Million cell updates/sec

US-10-083-853B-2

Sequence: 1 gttatgtatgaagaagcctca.....caattctgtgaagaagtaa 29921

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0  
Searched: 2185239 seqs, 1125999159 residues  
Word size : 0  
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database	ID	Score	Match	Length	DB	ID	Description
1: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*	1	652	2	1587	22	AAS04493	Human FCTR2 DNA pr
2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*	2	652	2	1728	22	AAS04496	Human PGDF DNA.
3: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*	3	652	2	1828	22	AAS04492	Human FCTR1 DNA pr
4: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*	4	652	2	3718	24	AAD25489	Human LP85 DNA #2.
5: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*	5	652	2	3736	21	AAD25488	Human LP85 DNA #1.
6: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*	6	601	2	1934	21	AAD00737	Human Platelet Der
7: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*	7	601	2	2253	21	AAD00738	Human Platelet Der
8: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*	8	601	2	3798	22	AAH46939	Human secreted pro
9: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*	9	601	2	4001	22	AAH46957	Human secreted pro
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23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*							
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
C 1	652	2	1587	22	AAS04493
C 2	652	2	1728	22	AAS04496
C 3	652	2	1828	22	AAS04492
C 4	652	2	3718	24	AAD25489
C 5	652	2	3736	21	AAD25488
C 6	601	2	1934	21	AAD00737
C 7	601	2	2253	21	AAD00738
C 8	601	2	3798	22	AAH46939
C 9	601	2	4001	22	AAH46957

10	499	1.7	2726	22	AAH46959	Human secreted pro
11	460	1.5	485	21	ABL63632	Breast cancer rela
C 12	377	1.3	1882	21	AAC81555	Human growth facto
C 13	377	1.3	1882	21	AAAS1541	SEQ. ID. 36 from W
C 14	377	1.3	1882	22	AAH47772	Human zvegff4 polyp
C 15	377	1.3	1882	24	ABQ73239	Human zvegff4 encod
C 16	377	1.3	3853	22	AAF24196	Human VEGF-G cDNA.
C 17	221	0.7	620	22	ABA08941	Human novel protei
C 18	221	0.7	1110	22	AAF24197	Human VEGF-G codin
C 19	221	0.7	1162	22	AAAS21336	Human cDNA sequenc
C 20	221	0.7	1162	24	ABL95717	Human angiogenesis
C 21	221	0.7	1162	24	ABL88228	Human PR04345 cDNA
C 22	221	0.7	1404	24	AAD25490	Human LP85 DNA #3.
C 23	220	0.6	462	22	AAS04496	Human FCTR5 DNA pr
C 24	185	0.6	360	21	AAD00739	Human Platelet Der
C 25	165	0.6	690	21	AAD00736	Human Platelet Der
C 26	155	0.5	2057	23	AAS73168	DNA encoding novel
C 27	155	0.5	2253	23	AAS73143	DNA encoding novel
28	155	0.5	2480	23	AAS69375	DNA encoding novel
29	155	0.5	2558	22	ABA15787	Human nervous syst
C 30	155	0.5	3303	23	AAS78786	DNA encoding novel
C 31	155	0.5	3303	23	AAAS1891	DNA encoding novel
C 32	155	0.5	3309	23	AAS72051	DNA encoding novel
C 33	155	0.5	3309	23	AAS78174	DNA encoding novel
C 34	155	0.5	3309	23	AAS78439	DNA encoding novel
C 35	155	0.5	3573	23	AAS69829	DNA encoding novel
C 36	155	0.5	3573	23	AAS70806	DNA encoding novel
C 37	155	0.5	3573	23	AAS87857	DNA encoding novel
C 38	155	0.5	3573	23	AAS92380	DNA encoding novel
39	155	0.5	3890	22	AAS27695	DNA encoding novel
40	155	0.5	3890	23	ABK42841	Genomic sequence #
C 41	155	0.5	3915	23	AAS78976	DNA encoding novel
C 42	155	0.5	3922	22	AAI98916	Human excretory re
C 43	155	0.5	3922	22	AAS30399	DNA encoding novel
44	155	0.5	3922	22	AAI04426	Human reproductive
45	155	0.5	3922	22	AAI63266	Human kidney relat

ALIGNMENTS

RESULT 1						
AAS04493/C						
ID	AAS04493	standard; DNA; 1587 BP				
XX						
AC	AAS04493;					
XX						
DT	07-SEP-2001	(first entry)				
XX						
DE	Human FCTR2 DNA present in clone 30664188.0.331.					
XX						
KW	Bone morphogenetic protein-1; BMP-1; vascular endothelial growth factor;					
KW	VEGF-E; platelet derived growth factor; PDGF; FCTR; hyperplasia; cancer;					
KW	neoplasia; anaemia; leukopenia; baldness; cardiovascular disorder;					
KW	fibrotic disorder; diabetic ulcer; obesity; hyperproliferation; human;					
KW	dysproliferation; neurodegenerative disorder; osteoarthritis; epilepsy;					
KW	inflammatory disorder; Graft versus host disease; coagulation; ds;					
KW	haemophilia; neural disorder; Parkinson's disease; Alzheimer's disease;					
KW	multiple sclerosis; Huntington's disease; amyotrophic lateral sclerosis;					
KW	peripheral neuropathy; acute brain injury.					
OS	Homo sapiens.					
XX						
FH	Key	Location/Qualifiers				
FT	CDS	540..938				
FT		/*tag= a				
FT		/product= "Human" FCTR2"				
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XX	W0200125437-A2.					
XX	12-APR-2001.					
XX						
PF	06-OCT-2000; 2000WO-US27671.					



XX PF 06-OCT-2000; 2000MO-US27671.  
 XX PR 07-OCT-1999; 99US-0158083.  
 PR 13-OCT-1999; 99US-0159231.  
 PR 04-JAN-2000; 2000US-0174485.  
 PR 03-MAR-2000; 2000US-0186707.  
 PR 10-MAR-2000; 2000US-0188250.  
 PR 08-AUG-2000; 2000US-0223879.  
 PR 12-SEP-2000; 2000US-0662783.  
 PR 20-SEP-2000; 2000US-0234082.  
 XX (CURA-) CURAGEN CORP.  
 XX PA Shimkets RA, Lichenstein H, Herrmann JL, Boldog FL, Minskoff S;  
 PI Jeffers M;  
 XX PI WPI; 2001-316172/33.  
 DR P-PSDB; AAU00704.  
 XX Novel growth factor polypeptides termed as FCTR polypeptides, useful  
 PT for treating cancer, cardiovascular and fibrotic diseases, diabetic  
 PT ulcers, wound healing and neuronal disorders  
 XX Disclosure; Fig 13; 171pp; English.  
 XX The sequence represents DNA encoding a protein related to bone  
 CC morphogenetic protein-1 (BMP-1), vascular endothelial growth factor  
 CC (VEGF-E) and platelet derived growth factor (PDGF). Polypeptides and  
 CC polynucleotides related to BMP-1, VEGF-E and PDGF are referred to as  
 CC FCTR polypeptides and nucleic acids. FCTR proteins are useful for treating  
 CC or preventing a disorder associated with aberrant expression, aberrant  
 CC processing, or aberrant physiological interactions of the proteins in a  
 CC mammal, where the disorder is characterised by insufficient or  
 CC ineffective growth of a cell or a tissue, e.g. hyperplasia or neoplasia.  
 CC The peptides and their associated nucleic acids are useful for both  
 CC promoting and inhibiting growth of cells and tissues and in treatment of  
 CC cancer, anaemia, leukopenia, baldness, for treating cardiovascular and  
 CC fibrotic disorders, diabetic ulcers, obesity, infectious diseases,  
 CC hyperproliferative and dysproliferative disorders, neurodegenerative  
 CC disorders, osteoarthritis, inflammatory disorders, graft versus host  
 CC disease, coagulation disorders such as haemophilia, and neural disorders  
 CC including Parkinson's disease, Alzheimer's disease, multiple sclerosis,  
 CC Huntington's disease, amyotrophic lateral sclerosis, peripheral  
 CC neuropathy, acute brain injury and epilepsy.  
 XX Sequence 1728 BP; 530 A; 364 C; 379 G; 455 T; 0 other;  
 SQ

Query Match 2.2%; Score 652; DB 22; Length 1728;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-188;  
 Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATATGTAGAAGCCTCATCTTTTGATTTTAAATATACAAAGATGCTTTCTTTAAGAGA 60  
 DB 1718 GTATATGTAGAAGCCTCATCTTTTGATTTTAAATATACAAAGATGCTTTCTTTAAGAGA 1659  
 QY 61 GCAAGATTCAAAATTTGTTTGTCTTCAAAATTTAAATTTATCTCTTAATTTT 120  
 DB 1658 GCAAGATTCAAAATTTGTTTGTCTTCAAAATTTAAATTTATCTCTTAATTTT 1599  
 QY 121 CTAAGACATGTTTTCATATATTTTGACCATCCCTTTATTTTGGCAAAGATTTTAAAGATCT 180  
 DB 1598 CTAAGACATGTTTTCATATATTTTGACCATCCCTTTATTTTGGCAAAGATTTTAAAGATCT 1539  
 QY 181 AACTCAACATATGTAGTCTCTGTTGACCTGCTTATATATACCAAAAAAATTTTAT 240  
 DB 1538 AACTCAACATATGTAGTCTCTGTTGACCTGCTTATATATACCAAAAAAATTTTAT 1479  
 QY 241 CTATATACATACATGATGAATATATTTCTGCTGTTTGTGTCATATATAACCTCAAC 300  
 DB 1478 CTATATACATACATGATGAATATATTTCTGCTGTTTGTGTCATATATAACCTCAAC 1419  
 QY 301 ACTATTATTAAATGCAATCCTATATTTCTTAGGTATAGAAGTTGATGATATACCTTTCTAC 360

DB 1418 ACTATTATTAAATGCAATCCTATATTTCTTAGGTATAGAAGTTGATGATATACCTTTCTAC 1359  
 QY 361 TTGCCATGGCATTAAACAAAGAGCTGAGACTCAGCAACCACTTGTGTTTCATTGCAATG 420  
 DB 1358 TTGCCATGGCATTAAACAAAGAGCTGAGACTCAGCAACCACTTGTGTTTCATTGCAATG 1299  
 QY 421 CAGGCTAGTAGTAAGTTTGTGTTCTGTTAGTAAAGGGTCTCTTATCTCACCCCTCTTAA 480  
 DB 1298 CAGGCTAGTAGTAAGTTTGTGTTCTGTTAGTAAAGGGTCTCTTATCTCACCCCTCTTAA 1239  
 QY 481 ACTAAAGTTCTTTTCAGGCTTAATGTAAGGATGTCACATCTCTTATCTCAGGTGGTCTT 540  
 DB 1238 ACTAAAGTTCTTTTCAGGCTTAATGTAAGGATGTCACATCTCTTATCTCAGGTGGTCTT 1179  
 QY 541 GAGCTCAGATACATAATCAGATCTTTCATGTTGATCCAACTGGAATGCAACTAGAGCCATG 600  
 DB 1178 GAGCTCAGATACATAATCAGATCTTTCATGTTGATCCAACTGGAATGCAACTAGAGCCATG 1119  
 QY 601 GTCTTAGCTCTACCCCTCTCTTGTGATGTGGCCAGGCTCAAACTGTATACCT 652  
 DB 1118 GTCTTAGCTCTACCCCTCTCTTGTGATGTGGCCAGGCTCAAACTGTATACCT 1067

RESULT 3  
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 ID AAS04492 standard; DNA; 1828 BP.  
 XX AC AAS04492;  
 XX DT 07-SEP-2001 (first entry)  
 XX DE Human FCTR1 DNA present in clone 30664188.0.99.  
 XX KW Bone morphogenetic protein-1; BMP-1; vascular endothelial growth factor;  
 KW VEGF-E; platelet derived growth factor; PDGF; FCTR; hyperplasia; cancer;  
 KW neoplasia; anaemia; leukopenia; baldness; cardiovascular disorder;  
 KW fibrotic disorder; diabetic ulcer; obesity; hyperproliferation; human;  
 KW dysproliferation; neurodegenerative disorder; osteoarthritis; epilepsy;  
 KW inflammatory disorder; Graft versus host disease; coagulation; ds;  
 KW haemophilia; neural disorder; Parkinson's disease; Huntington's disease;  
 KW multiple sclerosis; amyotrophic lateral sclerosis; peripheral neuropathy;  
 KW acute brain injury.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT CDS 182..1294  
 FT /tag= a  
 FT /product= "Human FCTR1"  
 FT sig\_peptide 182..250  
 FT /tag= b  
 FT mat\_peptide 251..1291  
 FT /tag= c  
 FT /product= "Mature human FCTR1"  
 XX WO2001125437-A2.  
 XX PN 12-APR-2001.  
 XX PD 06-OCT-2000; 2000MO-US27671.  
 XX PF 07-OCT-1999; 99US-0158083.  
 XX PR 13-OCT-1999; 99US-0159231.  
 PR 04-JAN-2000; 2000US-0174485.  
 PR 03-MAR-2000; 2000US-0186707.  
 PR 10-MAR-2000; 2000US-0188250.  
 PR 08-AUG-2000; 2000US-0223879.  
 PR 12-SEP-2000; 2000US-0662783.  
 PR 20-SEP-2000; 2000US-0234082.  
 XX (CURA-) CURAGEN CORP.  
 XX PA

PI Shimkets RA, Lichenstein H, Herrmann JL, Boldog FL, Minskoff S;  
PI Jeffers M;  
DR WPI: 2001-316172/33.  
DR P-PSDB; AAU00698.  
XX Novel growth factor polypeptides termed as FCTR polypeptides, useful  
PT for treating cancer, cardiovascular and fibrotic diseases, diabetic  
PT ulcers, wound healing and neuronal disorders  
XX  
PS Claim 11; Page 11-12; 171pp; English.  
XX  
CC The sequence represents DNA encoding a protein related to bone  
CC morphogenetic protein-1 (BMP-1), vascular endothelial growth factor  
CC (VEGF-E) and platelet derived growth factor (PDGF). Polypeptides and  
CC polynucleotides related to BMP-1, VEGF-E and PDGF are referred to as  
CC FCTR polypeptides and nucleic acids. FCTR proteins are useful for treating  
CC or preventing a disorder associated with aberrant expression, aberrant  
CC processing, or aberrant physiological interactions of the proteins in a  
CC mammal, where the disorder is characterized by insufficient or  
CC ineffective growth of a cell or a tissue, e.g. hyperplasia or neoplasia.  
CC The peptides and their associated nucleic acids are useful for both  
CC promoting and inhibiting growth of cells and tissues and in treatment of  
CC cancer, anemia, leukopenia, baldness, for treating cardiovascular and  
CC fibrotic disorders, diabetic ulcers, obesity, infectious diseases,  
CC hyperproliferative and dysproliferative disorders, neurodegenerative  
CC disorders, osteoarthritis, inflammatory disorders, Graft versus host  
CC disease, coagulation disorders such as haemophilia, and neural disorders  
CC including Parkinson's disease, Alzheimer's disease, multiple sclerosis,  
CC Huntington's disease, amyotrophic lateral sclerosis, peripheral  
CC neuropathy, acute brain injury and epilepsy.  
XX  
SQ Sequence 1828 BP; 572 A; 380 C; 385 G; 491 T; 0 other;  
Query Match 2.2%; Score 652; DB 22; Length 1828;  
Best Local Similarity 100.0%; Pred. No. 1.8e-188;  
Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 G T A T A G T A A G A A G C C C A T C T T T T G A T T T T A T A T A C A A G A G C T T C T T T A A G A G A 60  
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1758 G C A A G A T T C A A A T T G T T T G T G T T T C A A A T T T A A A T T A A T T A T C T C T A A A T T T 1699  
121 C T A A A G A C A T G T T C A T A T A T T G A C C A T C C C T T A T T T G C A A A G G A T T T A A G A G C T 180  
1698 C T A A A G A C A T G T T C A T A T A T T T G A C C A T C C C T T A T T T T G C A A A G G A T T T A A G A G C T 1639  
181 A A C T C A A A C A T A T G T A A G C T C T G G T G A C C T G G T T A T A T A T A C C A A A A A A C A T T T G A T 240  
1638 A A C T C A A C A T A T G T A A G C T C G G T G T A C C T G G T T A T A T A T A C C A A A A A A C A T T T G A T 1579  
241 C T A T A T A C A C A T A G A C A T G A A T A T A T T T C T G T G T G T T T G T G C A T A T A T A A C C T C A A C 300  
1578 C T A T A T A C A C A T A G A C A T G A A T A T A T T T C T G T G T G T T T G T G C A T A T A T A A C C T C A A C 1519  
301 A C T A T A T A A T G C A A T C C T A T A T T C T A G T A T A G A A G T G A T G A T A C C T T T C A C 360  
1518 A C T A T A T A A T G C A A T C C T A T A T T C T A G T A T A G A A G T G A T G A T A C C T T T C A C 1459  
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1458 T T G C C A T G C A T T A A C A A G C G T G A G A C T C A G A C C A C A C T T G T G T C A T T G C A T T G 1399  
421 C A G G C T A G T A A G T T G T G T G T G A G A A A G G C T C T A T A T C T A C C C C T C C T T A A 480  
1398 C A G G C T A G T A A G T T G T G T G T G A G A A A A G G G T C T A T A T C T C A C C C T C C T T A A 1339  
481 A C T A A A G C T T T T C A G G C T T A A T G T A A G G A T G T G C A C A T T C T A T C T A T C G A G G T G C T T 540  
1338 A C T A A A G G T T C T T C A G G C T T A A T G T A A G G A T G T G C A C A T T C T A T C T A T C G A G G T G C T T 1279

QY 541 GAGCTGCAGATACAAATCACATCGTTTCATGGTGGTGCATCCAACTGGATGTCAACTAGAGCCATG 600  
DB 1278 GAGCTGCAGATACAAATCACATCGTTTCATGGTGGTGCATCCAACTGGATGTCAACTAGAGCCATG 1219  
QY 601 GTCCTTAGCTCTACCCCTCTCTTTGATGTGGCCAGGCTCAAACTGTAATACCT 652  
DB 1218 GTCCTTAGCTCTACCCCTCTCTTTGATGTGGCCAGGCTCAAACTGTAATACCT 1167  
RESULT 4  
AAD25489/c  
ID AAD25489 standard; DNA; 3718 BP.  
XX  
AC AAD25489;  
DT 26-MAR-2002 (first entry)  
XX  
DE Human LP85 DNA #2.  
XX  
KW LP85; platelet-derived growth factor; PDGF; antinflammatory; vulnery;  
osteopathic; neuroprotective; tranquilliser; musculoskeletal disorder;  
MSD; therapy; bone growth; cartilage differentiation; wound healing;  
neuron growth; bone fracture; osteoporosis; osteopenia; arthritis;  
sarcopenia; periodontal disease; tissue atrophy; endocrine disorder;  
muscle loss; immobility; bone density; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
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FT /product= "Human LP85 protein"  
FT sig\_peptide 114..149  
FT /\*tag= b  
FT mat\_peptide 150..1205  
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FT /product= "Human mature LP85 protein"  
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XX WO200189450-A2.  
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XX 29-NOV-2001.  
PD  
XX  
XX 08-MAY-2001; 2001WO-US11755.  
PF  
XX  
XX 19-MAY-2000; 2000US-205424P.  
PR  
XX 11-JAN-2001; 2001US-261071P.  
PR  
XX 11-JAN-2001; 2001US-261076P.  
XX  
XX (ELIL ) LILLY & CO ELI.  
XX  
XX Beals JM, Gonzalez-Dewhitt PA, Hammond LJ, Lu J, Na S, Su EW;  
PI Witcher DR, Wroblewski VJ;  
XX  
XX WPI: 2002-083040/11.  
DR  
XX P-PSDB; AAEL15820.  
XX  
XX Analog of a platelet-derived growth factor homolog, LP85 useful for  
PT treating osteoporosis, arthritis, sarcopenia, wounds, has one or more  
PT amino acid substitutions which destroy the tripeptidyl sequence of  
PT native LP85  
XX  
XX Disclosure: Page 111-113; 117pp; English.  
PS  
XX  
XX The present invention relates to LP85, an analogue of platelet-derived  
CC growth factor (PDGF) homologue. Sequences of the invention are useful  
CC for the manufacture of a medicament for treating musculoskeletal disorder  
CC (MSD) which include promoting bone growth, cartilage differentiation and  
CC function, wound healing, neuron growth, preventing cartilage degradation  
CC or neuronal degeneration. They are useful for treating bone fractures,  
CC osteoporosis, osteopenia, arthritis, sarcopenia, periodontal disease,  
CC tissue atrophy, traumatised connective tissues, grafted connective  
CC tissues and/or transplanted organs, bone or muscle loss due to



XX	Key	Location/Qualifiers	
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FT		/*tag= b	
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FT		/product= "Human mature LP85 protein"	
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XX	29-NOV-2001.		
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XX			
XX	08-MAY-2001; 2001WO-US11755.		
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PR	19-MAY-2000; 2000US-205424P.		
PR	11-JAN-2001; 2001US-261071P.		
PR	11-JAN-2001; 2001US-261076P.		
XX			
XX	(ELIL ) LILLY & CO ELI.		
XX			
PI	Beals JM, Gonzalez-Dewhitt PA, Hammond LJ, Lu J, Na S, Su EW;		
PI	Witcher DR, Wroblewski VJ;		
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XX	WPI; 2002-083040/11.		
DR	P-PSDB; AAE15819.		
XX			
DR	Analog of a platelet-derived growth factor homolog, LP85 useful for		
PT	treating osteoporosis, arthritis, sarcopenia, wounds, has one or more		
PT	amino acid substitutions which destroy the tripeptidyl sequence of		
PT	native LP85		
XX			
PS	Disclosure; Page 106-109; 117pp; English.		
XX			
CC	The present invention relates to LP85, an analogue of platelet-derived		
CC	growth factor (PDGF) homologue. Sequences of the invention are useful		
CC	for the manufacture of a medicament for treating musculoskeletal disorder		
CC	(MSD) which include promoting bone growth, cartilage differentiation and		
CC	function, wound healing, neuron growth, preventing cartilage degradation		
CC	or neuronal degeneration. They are useful for treating bone fractures,		
CC	osteoporosis, osteopenia, arthritis, sarcopenia, periodontal disease,		
CC	tissue atrophy, traumatised connective tissues, grafted connective		
CC	tissues and/or transplanted organs, bone or muscle loss due to		
CC	malnigancy, endocrine disorders and immobility. They are also used		
CC	for prophylactically increasing or maintaining bone density in a		
CC	mammal. The present sequence is a DNA encoding human LP85 protein.		
XX			
SQ	Sequence 3736 BP; 1164 A; 736 C; 718 G; 1118 T; 0 other;		

QY	1	GTATATGTAAGAAAGCCTCATCTTTTGTATTTTAAATATACAAGATGCTTTCTTTAAGAGA	60
Db	1750	GTATATGTAAGAAAGCCTCATCTTTTGTATTTTAAATATACAAGATGCTTTCTTTAAGAGA	1691
QY	61	GCAAGATTCAAAATCTGTTTGTCTTTCAAAATTTAAAAATAAATTTATCTCCCTAAATTTT	120
Db	1690	GCAAGATTCAAAATCTGTTTGTCTTTCAAAATTTAAAAATAAATTTATCTCCCTAAATTTT	1631
QY	121	CTAAGACATGTTTCATATATTGACATCCCTTATTTGGCAAGAGATTTTAAAGAGTCT	180
Db	1630	CTAAGACATGTTTCATATATTGACATCCCTTATTTGGCAAGAGATTTTAAAGAGTCT	1571
QY	181	AACTCAAAACATATGTAAGCTCTGGTGACTGGTTATATATACCAAAAAACATTTTGAT	240
Db	1570	AACTCAAAACATATGTAAGCTCTGGTGACTGGTTATATATACCAAAAAACATTTTGAT	1511
QY	241	CTATATACACATAGACATGAATATATTCTCTGCTGCTTGTGTCATATATAACCTCAAC	300



XX AC AAD00738;  
XX XX  
DT 08-SEP-2000 (first entry)  
XX DE Human Platelet-Derived Growth Factor (PDGF)-D encoding complete cDNA.  
XX KW Platelet-Derived Growth Factor-D; PDGF-D; human; cytosolic; vulnary;  
KW VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;  
KW proliferative; activator; proliferation; differentiation; motility;  
KW growth; PDGF-D receptor; antagonist; tissue remodelling; treat;  
KW atherosclerosis; wound; metastasis; ss.  
XX OS Homo sapiens.  
XX XX  
XX FH Location/Qualifiers  
XX CDS 176..1288  
XX FT /tag= a  
XX FT /product= "Human PDGF-D protein"  
XX FT /note= "platelet derived growth factor"  
XX PN WO200027879-A1  
XX XX  
XX PD 18-MAY-2000.  
XX XX  
XX PF 10-NOV-1999; 99WO-US26462.  
XX XX  
XX PR 10-NOV-1998; 98US-0107852.  
XX PR 28-DEC-1998; 98US-0113997.  
XX PR 26-AUG-1999; 99US-0150604.  
XX PR 04-OCT-1999; 99US-0157108.  
XX PR 05-OCT-1999; 99US-0157756.  
XX XX  
XX PA (LUDM-) LUDWIG INST CANCER RES.  
XX PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.  
XX XX  
XX PI Eriksson U, Aase K, Ponten A, Lee X, Uutela M, Alitalo K;  
XX PI Oestman A, Heldin C;  
XX XX  
XX DR WPI: 2000-376495/32.  
XX DR P-PSDB; AAY71130.  
XX XX  
XX PT Novel polynucleotides encoding a novel growth factor of cells  
XX PT expressing a platelet-derived growth factor, useful for diagnostic and  
XX PT therapeutic applications, e.g. concerning cancer.  
XX XX  
XX PS Claim 1; Fig 7, 11pp; English.  
XX XX  
XX CC The present sequence is the complete cDNA encoding human platelet derived  
XX CC growth factor (PDGF)-D, formally known as Vascular Endothelial Growth  
XX CC Factor (VEGF)-G. It is derived from human fetal lung lambda gt10 cDNA  
XX CC library. It belongs to the VEGF/PDGF family. It functions as an activator  
XX CC of proliferation, differentiation, growth and motility of cells, that  
XX CC express PDGF-D receptor. This sequence is useful for inhibiting the  
XX CC growth of tumours, that express PDGF-D. Expression of PDGF-D and its  
XX CC proteolytic cleavage for generating an activated truncated form is useful  
XX CC for regulating receptor binding specificity of PDGF-D. PDGF-D antagonist  
XX CC is useful for inhibiting tissue remodelling during the invasion of  
XX CC tumour cells into normal cells. PDGF-D may be used to treat wounds,  
XX CC atherosclerosis, metastasis and migration of smooth muscle cells.  
XX XX  
XX SQ Sequence 2253 BP; 701 A; 464 C; 490 G; 598 T; 0 other;  
XX XX  
XX Query Match 2.0%; Score 601; DB 21; Length 2253;  
XX Best Local Similarity 99.8%; Pred. No. 5.1e-173;  
XX Matches 651; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX XX  
XX QY 1 GTATGCTAGAGAGCGCTCATCTTTGATTTTAAATATACAGATGCTTTCTTTAAGAGA 60  
XX |||||||  
XX DB 1812 GTATGCTAGAGAGCGCTCATCTTTGATTTTAAATATACAGATGCTTTCTTTAAGAGA 1753  
XX |||||||  
XX QY 61 GCAAGATTCAAAATGTTTGTGTTTCAAAATTTAAATTTATATCTCCCTAAATTTT 120  
XX |||||||

Db 1752 GCAAGATTCAAAATGTTTGTGTTTCAAAATTTAAATTTATATCTCCCTAAATTTT 1693  
QY 121 CTAAGACATGTTTTCATATATTTGACCATCCCTTATTTTGGCAAGGATTTTAAAGAGTCT 180  
Db 1692 CTAAGACATGTTTTCATATATTTGACCATCCCTTATTTTGGCAAGGATTTTAAAGAGTCT 1633  
QY 181 AACTCAACATATGTAAGCTCTGCTGTAACCTGTTATATATACCAAAAAAACAATTTGAT 240  
Db 1632 AACTCAACATATGTAAGCTCTGCTGTAACCTGTTATATATACCAAAAAAACAATTTGAT 1573  
QY 241 CTAATACACATAGACATGAATATATTTCTGTGTGTGTTGTCATATATATAAAGCTCAAC 300  
Db 1572 CTAATACACATAGACATGAATATATTTCTGTGTGTGTTGTCATATATATAAAGCTCAAC 1513  
QY 301 ACTATTATTAATGCAATCTATATTTCTTAGGTATAGAACTTCATGATATACCTTTCTAC 360  
Db 1512 ACTATTATTAATGCAATCTATATTTCTTAGGTATAGAACTTCATGATATACCTTTCTAC 1453  
QY 361 TTGCCATGCGATTAAACAAAGGCTGAGACTCAGCAACCACTTGTGTTTCATTGCAATG 420  
Db 1452 TTGCCATGCGATTAAACAAAGGCTGAGACTCAGCAACCACTTGTGTTTCATTGCAATG 1393  
QY 421 CAGGCTAGTAGTAAGTTTGGTCTGCTAGGAAAGGCTCTTATCTCAACCTCCCTTAA 480  
Db 1392 CAGGCTAGTAGTAAGTTTGGTCTGCTAGGAAAGGCTCTTATCTCAACCTCCCTTAA 1333  
QY 481 ACTAAAGGTTCTTTTTCAGGCTTAATGTAAGGATGTCACATCTCTTATCGAGGTGGTCTT 540  
Db 1332 ACTAAAGGTTCTTTTTCAGGCTTAATGTAAGGATGTCACATCTCTTATCGAGGTGGTCTT 1273  
QY 541 GAGCTGCAGATACATACATCTGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG 600  
Db 1272 GAGCTGCAGATACATACATCTGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG 1213  
QY 601 GTCTTAGTCTACCCCTCTCTTGTGATGTGCGCAGGCTCAACCTGTAATACCT 652  
Db 1212 GTCTTAGTCTACCCCTCTCTTGTGATGTGCGCAGGCTCAACCTGTAATACCT 1161  
XX XX  
XX RESULT 8  
XX AAH46939/c  
XX ID AAH46939 standard; cDNA; 3798 BP.  
XX AC AAH46939;  
XX XX  
XX DT 25-SEP-2001 (first entry)  
XX XX  
XX DE Human secreted protein encoding. cDNA (clone Id HGCNC48).  
XX KW Secreted protein; immunosuppressive; antiarthritic; antirheumatic;  
XX KW antiproliferative; cytosolic; cardiac; vasotropic; cerebroprotective;  
XX KW neurotropic; neuroprotective; antibacterial; virucide; fungicide; human;  
XX KW Ophthalmological; gene therapy; ss.  
XX OS Homo sapiens.  
XX XX  
XX PN WO200155430-A1.  
XX XX  
XX PD 02-AUG-2001.  
XX XX  
XX PF 17-JAN-2001; 2001WO-US01431.  
XX XX  
XX PR 31-JAN-2000; 2000US-0179065.  
XX PR 04-FEB-2000; 2000US-0180628.  
XX PR 12-SEP-2000; 2000US-0231968.  
XX XX  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX XX  
XX PI Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;  
XX PI Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fiscella M;  
XX PI Ni J, Ruben SM, Barash SC;  
XX XX  
XX DR WPI: 2001-476220/51.

DR P-PSDB; AAB85529.

XX 17 isolated nucleic acid molecules encoding human secreted proteins,  
PT used to preventing, treating or ameliorating a medical condition -  
PT  
XX  
PS Claim 1; Page 417-418; 482pp; English.

XX The invention provides novel human secreted proteins and polynucleotides  
CC encoding them. The secreted proteins can be expressed by standard  
CC recombinant methodology. The secreted proteins and polynucleotides are  
CC used to prevent, treat or ameliorate a medical condition in e.g. humans,  
CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can  
CC also be used in diagnosing a pathological condition. The antibodies to  
CC the proteins can also be used in alleviating symptoms associated with the  
CC disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme  
CC linked immunosorbent assays (ELISA). Disorders which are diagnosed or  
CC treated include autoimmune diseases e.g. rheumatoid arthritis,  
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,  
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
CC e.g. cerebral ischemia, angioneurosis, nervous system disorders e.g.  
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and  
CC ocular disorders e.g. corneal infection. The polypeptides can also be  
CC used to aid wound healing and epithelial cell proliferation, to prevent  
CC skin aging due to sunburn, to maintain organs before transplantation, for  
CC supporting cell culture of primary tissues, to regenerate tissues and in  
CC chemotaxis. The polypeptides can also be used as a food additive or  
CC preservative to increase or decrease storage capabilities. The present  
CC sequence represents a human secreted protein encoding cDNA.

XX Sequence 3798 BP; 1189 A; 749 C; 737 G; 1123 T; 0 other;

Query Match 2.0%; Score 601; DB 22; Length 3798;  
Best Local Similarity 99.8%; Pred. No. 4.6e-173;  
Matches 651; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTATATGTAAGAAAGCCCTCATCTTTTGATTTTATATACAGATGCTTTCTTTAGAGA 60  
DB 1802 GTATATGTAAGAAAGCCCTCATCTTTTGATTTTATATACAGATGCTTTCTTTAGAGA 1743

QY 61 GCAAGATTCAAAATGTTTGTGTTTCAAAATTTTAAATTAATTTATCTCTCAATTTT 120  
DB 1742 GCAAGATTCAAAATGTTTGTGTTTCAAAATTTTAAATTAATTTATCTCTCAATTTT 1683

QY 121 CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAGAGATTTTAAAGATCT 180  
DB 1682 CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAGAGATTTTAAAGATCT 1623

QY 181 AACTCAACATATGTAAGCTCTGGTGACCTGGTTATATATACCAAAAAACATTTGAT 240  
DB 1622 AACTCAACATATGTAAGCTCTGGTGACCTGGTTATATATACCAAAAAACATTTGAT 1563

QY 241 CTAATACACATAGACATGAATATATTTCTGTGTGTTTGGCATATATACCTCAAC 300  
DB 1562 CTAATACACATAGACATGAATATATTTCTGTGTGTTTGGCATATATACCTCAAC 1503

QY 301 ACTATTATTAAGCAATCCTATATCTTAGTATAGAGTTGATGATACCTTTCTAC 360  
DB 1502 ACTATTATTAAGCAATCCTATATCTTAGTATAGAGTTGATGATACCTTTCTAC 1443

QY 361 TTGCCATGCATTAACAAGCAAGCTGAGACTCAGCAACCACTTGTCTTATTCATG 420  
DB 1442 TTGCCATGCATTAACAAGCAAGCTGAGACTCAGCAACCACTTGTCTTATTCATG 1383

QY 421 CAGGCTAGTAGTAAGTTGGTGTGGTGGAGAAAGGGTCTTATCTCACCTCCTTAA 480  
DB 1382 CAGGCTAGTAGTAAGTTGGTGTGGTGGAGAAAGGGTCTTATCTCACCTCCTTAA 1323

QY 481 ACTAAGGTCTTTTCAGGCTTAATGTAAGGATGTCACATCTCTTATCGAGGTGGTCTT 540  
DB 1322 ACTAAGGTCTTTTCAGGCTTAATGTAAGGATGTCACATCTCTTATCGAGGTGGTCTT 1263

QY 541 GAGCTGCAGATACATACATCGTTTCATGGTTCATCCCACTGGATGCTCAACTAGACCCATG 600  
DB 1123 GAGCTGCAGATACATACATCGTTTCATGGTTCATCCCACTGGATGCTCAACTAGACCCATG 600

DB 1262 GAGCTGCAGATACATACATCGTTTCATGGTTCATCCCACTGGATGCTCAACTAGACCCATG 1203

QY 601 GTCCTAGCTCTACCCCTCTCTTGTGTCGCCAGGCTCAAACTGTAATACCT 652  
DB 1202 GTCCTAGCTCTACCCCTCTCTTGTGTCGCCAGGCTCAAACTGTAATACCT 1151

RESULT 9

ID AAH46957/c  
AAH46957 standard; cDNA; 4001 BP.

XX  
AC AAH46957;  
XX 25-SEP-2001 (first entry)  
XX Human secreted protein encoding cDNA (clone Id HE8TY90).

DE Secreted protein; immunosuppressive; antiarthritic; antirheumatic;  
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;  
KW neurotropic; neuroprotective; antibacterial; virucide; fungicide; human;  
KW ophthalmological; gene therapy; ss.

XX Homo sapiens.

OS  
XX WO200155430-A1.  
XX 02-AUG-2001.  
XX 17-JAN-2001; 2001WO-US01431.  
XX 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 12-SEP-2000; 2000US-0231968.  
XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;  
PI Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fiscella M;  
PI Ni J, Ruben SM, Barash SC;  
XX WPI: 2001-476220/51.  
DR P-PSDB; AAB85547.

XX 17 isolated nucleic acid molecules encoding human secreted proteins,  
PT used to preventing, treating or ameliorating a medical condition -  
PT  
XX Claim 1; Page 430-432; 482pp; English.

XX The invention provides novel human secreted proteins and polynucleotides  
CC encoding them. The secreted proteins can be expressed by standard  
CC recombinant methodology. The secreted proteins and polynucleotides are  
CC used to prevent, treat or ameliorate a medical condition in e.g. humans,  
CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can  
CC also be used in diagnosing a pathological condition. The antibodies to  
CC the proteins can also be used in alleviating symptoms associated with the  
CC disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme  
CC linked immunosorbent assays (ELISA). Disorders which are diagnosed or  
CC treated include autoimmune diseases e.g. rheumatoid arthritis,  
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,  
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
CC e.g. cerebral ischemia, angioneurosis, nervous system disorders e.g.  
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and  
CC ocular disorders e.g. corneal infection. The polypeptides can also be  
CC used to aid wound healing and epithelial cell proliferation, to prevent  
CC skin aging due to sunburn, to maintain organs before transplantation, for  
CC supporting cell culture of primary tissues, to regenerate tissues and in  
CC chemotaxis. The polypeptides can also be used as a food additive or  
CC preservative to increase or decrease storage capabilities. The present  
CC sequence represents a human secreted protein encoding cDNA.

XX Sequence 4001 BP; 1218 A; 823 C; 796 G; 1156 T; 8 other;

Query Match 2.0%; Score 601; DB 22; Length 4001;

[illegible][illegible]

Db 2422 CAGGCTAGTAGTAAGTTTGGTTGCTGTAGGAAAGGCTCTTATCTCACCTCCTTAA 2481  
Qy 481 ACTAAGAGTCTTTTACAGGCTTAATGTAAGGATGTCACATCTCTTATCGAGGTGCTTT 540  
Db 2482 ACTATAGTCTTTTACAGGCTTAATGTAAGGATGTCACATCTCTTATCGAGGTGCTTT 2541  
Qy 541 GAGCTGCAGATACAATACATCATGTTTCATGTTGATGCCAAGTGGATGTCACACTAGAGCCATG 600  
Db 2542 GAGCTGCAGATACAATACATCATGTTTCATGTTGATGCCAAGTGGATGTCACACTAGAGCCATG 2601  
Qy 601 GTCCTAGCTCTACCCCTCTCTTGTAGTGCGCCAGGCTCAAACTGTAATACCT 652  
Db 2602 GTCCTAGCTCTACCCCTCTCTTGTAGTGCGCCAGGCTCAAACTGTAATACCT 2653

RESULT 11

ABL63632  
ID ABL63632 standard; DNA; 485 BP.

XX ABL63632;

XX 15-MAY-2002 (first entry)

XX Breast cancer related gene sequence SEQ ID NO:1969.

KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;  
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;  
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;  
KW gene; ds.

XX Homo sapiens.

XX WO200194629-A2.

XX 13-DEC-2001.

XX 30-MAY-2001; 2001WO-US10838.

PR 05-JUN-2000; 2000US-209473P.

PR 18-SEP-2000; 2000US-209531P.

PR 18-SEP-2000; 2000US-233131P.

PR 20-SEP-2000; 2000US-233617P.

PR 20-SEP-2000; 2000US-234009P.

PR 20-SEP-2000; 2000US-234034P.

PR 22-SEP-2000; 2000US-234052P.

PR 22-SEP-2000; 2000US-234509P.

PR 22-SEP-2000; 2000US-234567P.

PR 25-SEP-2000; 2000US-234923P.

PR 25-SEP-2000; 2000US-234924P.

PR 25-SEP-2000; 2000US-235077P.

PR 25-SEP-2000; 2000US-235082P.

PR 25-SEP-2000; 2000US-235134P.

PR 25-SEP-2000; 2000US-235280P.

PR 26-SEP-2000; 2000US-235637P.

PR 26-SEP-2000; 2000US-235638P.

PR 27-SEP-2000; 2000US-235711P.

PR 27-SEP-2000; 2000US-235720P.

PR 27-SEP-2000; 2000US-235840P.

PR 02-OCT-2000; 2000US-237316P.  
PR 03-OCT-2000; 2000US-237425P.  
PR 03-OCT-2000; 2000US-237598P.  
PR 03-OCT-2000; 2000US-237604P.  
PR 03-OCT-2000; 2000US-237606P.  
PR 03-OCT-2000; 2000US-237608P.  
PR 01-NOV-2000; 2000US-244867P.  
PR 01-NOV-2000; 2000US-245084P.  
PA (AVAL-) AVALON PHARM.  
XX  
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;  
PI Soppet DR, Weaver Z;  
XX  
XX WPI; 2002-188264/24.  
XX  
XX Screening for anti-neoplastic agent involves exposing cells to a  
PT chemical agent to be tested for anti-neoplastic activity, and  
PT determining a change in expression of a gene of a signature gene set -  
XX  
XX Claim 1; SEQ ID 1969; 44pp; English.  
XX  
XX The present invention describes a method (M1) for screening for an  
CC anti-neoplastic agent. The method involves exposing cells to a chemical  
CC agent to be tested for anti-neoplastic activity, determining a change in  
CC expression of at least one gene (I) of a signature gene set, where (I)  
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664  
CC to ABL70110), or is at least 95% identical to (S), where a change in  
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic  
CC activity and can be used in gene therapy. M1 can be used for screening  
CC an anti-neoplastic agent, and can be used for producing a product which  
CC is the data collected with respect to the anti-neoplastic agent as a  
CC result of M1, and the data is sufficient to convey the chemical  
CC structure and/or properties of the agent. M1 can be used in the  
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,  
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,  
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,  
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine  
CC carcinoma, papillary carcinoma and Wilm's tumour.  
XX  
XX Sequence 485 BP; 161 A; 72 C; 75 G; 177 T; 0 other;  
XX  
Query Match 1.5%; Score 460; DB 24; Length 485;  
Best Local Similarity 100.0%; Pred. No. 4e-130;  
Matches 460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GTATATGTAAGAAAGCCCTCATCTTTTGGATTTTAAATATACAGATGCTTTCTTTAAGAGA 60  
Db 26 GTATATGTAAGAAAGCCCTCATCTTTTGGATTTTAAATATACAGATGCTTTCTTTAAGAGA 85  
Qy 61 GCAAGATTCAAAATTTGTTTGTGTTTCAAAATTTAAATAATTTATCTCTAAATTTT 120  
Db 86 GCAAGATTCAAAATTTGTTTGTGTTTCAAAATTTAAATAATTTATCTCTAAATTTT 145  
Qy 121 CTAAGACATGTTTCATATATATTTGACCATCCCTTATTTGGCAAGAGATTTTAAGAGTCT 180  
Db 146 CTAAGACATGTTTCATATATATTTGACCATCCCTTATTTGGCAAGAGATTTTAAGAGTCT 205  
Qy 181 AACTCAACATATGTAAGCTCTGTTGTTACCTGTTATATATACCAAAAAACATTTGAT 240  
Db 206 AACTCAACATATGTAAGCTCTGTTGTTACCTGTTATATATACCAAAAAACATTTGAT 265  
Qy 241 CTATATACATAGACATGAATATATTTCTGTGTGTTTGTGCATATATAACCTCAAAAC 300  
Db 266 CTATATACATAGACATGAATATATTTCTGTGTGTTTGTGCATATATAACCTCAAAAC 325  
Qy 301 ACTATATTAAATGCAATCCCTATATCTTAGGTATAGAGTTGATGATATACCTTTCTAC 360  
Db 326 ACTATATTAAATGCAATCCCTATATCTTAGGTATAGAGTTGATGATATACCTTTCTAC 385  
Qy 361 TTGCCATGGCATTACAAGCAAGGCTGAGACTGACCACTGCTGTTTCATTGCTATG 420  
Db 386 TTGCCATGGCATTACAAGCAAGGCTGAGACTGACCACTGCTGTTTCATTGCTATG 445

QY 421 CAGGCTAGTAGTAAGTTTGGTTCGCTGGTAGGAAAGGGTC 460  
|||||  
Db 446 CAGGCTAGTAGTAAGTTTGGTTCGCTGGTAGGAAAGGGTC 485

RESULT 12  
AAC81555/c  
ID AAC81555 standard; cDNA; 1882 BP.

XX AAC81555;  
XX  
XX 09-MAR-2001 (first entry)  
XX  
XX Human growth factor homologue zveg4 cDNA, SEQ ID NO:1.

XX Human; zveg4; growth factor homologue; VEGF/PDGF family;  
XX CUB domain; PDGF-like activity; mitogenic; osteogenic;  
KW neovascularisation; tissue repair; proliferation; differentiation;  
KW liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;  
KW periodontal disease; bone fracture; wound healing; vulnery; ischaemia;  
KW immunomodulation; hepatic; chromosome 11q22.3-23.1; ss.

XX Homo sapiens.

OS  
XX WO2000066736-A1.

XX  
XX 09-NOV-2000.

XX  
XX 03-MAY-2000; 2000WO-US40047.

XX  
XX 03-MAY-1999; 99US-0304216.

PR 10-NOV-1999; 99US-0164463.

PR 04-FEB-2000; 2000US-0180169.

XX (ZYMO ) ZYMOGENETICS INC.

PA Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;

PI WPI: 2000-687541/67.

XX P-PSDB; AAB48653.

XX Growth factor homologs and the nucleic acids that encode them, useful

XX e.g. for treating liver damage, ischemia, multiple sclerosis and

XX Alzheimer's disease -

XX Claim 35; Page 106-110; 143pp; English.

XX The invention relates to the human growth factor homologue zveg4  
XX (AAB48653), and nucleic acids encoding it (AAC81555). Zveg4 is a member  
XX of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial  
XX growth factor) family. Zveg4 has a growth factor domain (AAB48654)  
XX characterised by a PDGF cysteine knot structure, and a CUB domain  
XX (AAB48655) which has a beta barrel structure. Zveg4 has PDGF-like  
XX activity, having mitogenic activity on fibroblasts, vascular smooth  
XX muscle cells and pericytes, and has also been shown to stimulate bone  
XX growth. The invention also relates to fusion proteins comprising human  
XX zveg4 or fragments thereof, particularly human zveg4/human zveg3  
XX fusions; expression constructs and host cells comprising human zveg4  
XX nucleic acids; the recombinant expression of human zveg4; an antibody  
XX which binds to human zveg4 or a fragment thereof; a method of activating  
XX a cell-surface PDGF receptor using a zveg4-derived polypeptide; a  
XX method of modulating the proliferation, differentiation, migration or  
XX metabolism of bone cells, comprising exposing bone cells to  
XX zveg4-derived polypeptides; and a method of detecting a genetic  
XX abnormality in the zveg4 gene of a patient. Zveg4 proteins and derived  
XX fragments may be used to stimulate tissue development or repair, or  
XX cellular differentiation or proliferation. They are particularly used for  
XX the treatment or repair of liver damage, and may also be used to  
XX modulate neurite growth (e.g., in the treatment of Alzheimer's disease or  
XX multiple sclerosis). Due to their osteogenic activity, they may be used  
XX in the treatment of periodontal disease and fractures. They may also be  
XX used to enhance expansion and mobilisation of haematopoietic stem cells

PR 06-JUL-1999; 99US-0142576.  
PR 21-OCT-1999; 99US-0161653.  
PR 12-NOV-1999; 99US-0165255.  
PA (ZYMO ) ZYMOGENETICS INC.  
XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;  
PI Gilbertson DG, West JW;  
XX WPI; 2000-423420/36.  
DR P-PSDB; AAY96864.  
XX Novel zveg3 polypeptides and nucleotides encoding them useful for  
PT stimulating growth of smooth muscle cells and fibroblasts comprising an  
PT epitope bearing portion of a specific amino acid sequence  
XX  
PS Disclosure; Page 161-164; 173pp; English.  
XX  
CC Polypeptides comprising an epitope-bearing portion human or murine  
CC ZVEGF3 (vascular endothelial growth factor homologue) are claimed. The  
CC growth factors comprise a growth factor domain and a CUB domain (generic  
CC sequence motifs are shown in AAY96859 and AAY96860). The growth factor  
CC domain is characterized by an arrangement of cysteine residues and  
CC beta-strands that is characteristic of the "cysteine knot" structure of  
CC the platelet-derived growth factor (PDGF) family. The CUB domain shows  
CC homology to CUB domains in neurophilins, human bone morphogenetic  
CC protein-1, porcine seminal plasma protein, bovine acidic seminal fluid  
CC protein and Xenopus laevis tolloid-like protein. Structural analysis and  
CC homology predict that ZVEGF3 polypeptides complex with a second  
CC polypeptide to form multimeric proteins. The human zveg3 gene has been  
CC mapped to chromosome 4q28.3. ZVEGF3 is useful for stimulating the growth  
CC of fibroblasts or smooth muscle cells, for activating cell surface  
CC PDGF-alpha receptor and for inhibiting PDGF-alpha receptor mediated  
CC cellular processes. ZVEGF3 is useful for regulating (post-development)  
CC organ growth, regeneration and maintenance, as well as tissue  
CC maintenance and repair processes. ZVEGF3 antagonists are useful for  
CC treating cancer, rheumatoid arthritis, diabetic retinopathy, ischemic  
CC limb disease, peripheral vascular disease, myocardial ischemia, vascular  
CC intimal hyperplasia, atherosclerosis, wound healing, chronic liver  
CC disease and haemangioma formation. ZVEGF3 can also be used to modulate  
CC neurite growth and development of the nervous system, and for treating  
CC neurodegenerative diseases.  
XX  
SQ Sequence 1882 BP; 566 A; 407 C; 430 G; 479 T; 0 other;

Query Match  
Best Local Similarity 1.3%; Score 377; DB 21; Length 1882;  
Matches 427; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 225 AAAAAAACATTGATCTATATACATAGACATGAATATATTTCTGTGTGTTGTGC 284  
DB 1638 AAAAAAACATTGATCTATATACATAGACATGAATATATTTCTGTGTGTTGTGC 1579  
QY 285 ATATATACCTCAACACTATTATTAATGCAATCCTATATCTTAGTATAGAGTTGA 344  
DB 1578 ATATATACCTCAACACTATTATTAATGCAATCCTATATCTTAGTATAGAGTTGA 1519  
QY 345 TGATATACCTTCTTACCTGCCATTACAAAGCAAGCTGAGACTCAGCAACCACT 404  
DB 1518 TGATATACCTTCTTACCTGCCATTACAAAGCAAGCTGAGACTCAGCAACCACT 1459  
QY 405 TGTGTTTCATTGCTGAGGCTAGTAGTAAGTTTGTGTTGTTGAGGAAAGGCTCTCTT 464  
DB 1458 TGTGTTTCATTGCTGAGGCTAGTAGTAAGTTTGTGTTGTTGAGGAAAGGCTCTCTT 1399  
QY 465 ATCTACCCCTCTTAACCTAAGGTTCTTTCCAGGCTTAATTAAGGATGTCACATCTC 524  
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QY 585 GTCRAACTAGAGCCATGGTCTTTAGCTCTACCCCTCTCTTTGATGTGGCCAGGCTCAAACTG 644  
DB 1278 GTCRAACTAGAGCCATGGTCTTTAGCTCTACCCCTCTCTTTGATGTGGCCAGGCTCAAACTG 1219  
QY 645 TAATACCT 652  
DB 1218 TAATACCT 1211  
RESULT 14  
AAH47772/C  
ID AAH47772 standard; cDNA; 1882 BP.  
AC XX  
AC AAH47772;  
XX  
DT 07-JAN-2002 (first entry)  
XX  
DE Human zveg4 polypeptide encoding cDNA.  
XX  
KW zveg4; bone; ligament; cartilage; osteoblast; osteoclast; chondrocyte;  
KW bone cancer; osteonecrosis; bone defect; osteogenesis; osteoporosis;  
KW osteopathic; vulnery; human; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 226..1338  
FT /\*tag= a  
FT /\*product= "zveg4 protein"  
FT sig\_peptide 226..279  
FT /\*tag= b  
FT mat\_peptide 280..1335  
FT /\*tag= c  
XX  
XX WO200157083-A1.  
PN 09-AUG-2001.  
PD  
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PP 03-MAY-2000; 2000WO-US12095.  
XX  
PR 04-FEB-2000; 2000US-180169P.  
PR 31-MAR-2000; 2000US-0540224.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX  
PI Gilbertson DG, Hart CE;  
XX  
DR WPI; 2001-611088/70.  
DR P-PSDB; AAG65601.  
XX  
PT Use of zveg4 polypeptide for promoting bone, ligament or cartilage  
PT growth in mammal at site of fracture, implant, and bone graft, and for  
PT promoting growth or differentiation of osteoblasts, chondrocytes in  
PT culture  
XX  
PS Example 1; Page 44-47; 57pp; English.  
XX  
CC The invention relates to the use of zveg4 polypeptide for promoting  
CC bone, ligament or cartilage growth in a mammal, and for promoting  
CC proliferation or differentiation of osteoblasts, osteoclasts,  
CC chondrocytes or bone marrow stem cells in culture. For promoting  
CC cartilage growth, chondrocytes are cultured ex vivo in presence of the  
CC zveg4 polypeptide and then placed into mammal where cartilage is to be  
CC grown. Zveg4 polypeptide is useful for promoting growth of bone,  
CC ligament or cartilage in a mammal at a site of bony defect such as  
CC fracture, bone graft, implant or periodontal pocket, in humans and non-  
CC human animals such as domestic animals including livestock and companion  
CC animals. Zveg4 is used for promoting growth of bone, ligament, or  
CC cartilage in conditions of bone defects following therapeutic treatments  
CC of bone cancers or other conditions characterized by increased bone loss  
CC or decreased bone formation, or elevation of peak bone mass in pre-  
CC menopausal woman. It is also useful for healing bone following radiation



PD	30-MAY-2002.	1
XX		
PF	14-MAR-2001; 2001US-0808972.	1
XX		
PR	03-MAY-1999; 99US-132250P.	1

PR 04-FEB-2000; 2000US-180169P;

PR 26-SEP-2000; 2000US-233293P.  
PR 03-MAY-2000; 2000US-0564595.

XX  
DA / ЧАРТ / ЧАРТ С Е

PA (TOPO/) TOPOUZIS S.  
PA (CIPBA) CILBERTSON D. C.

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DR P-PSDB; ABP51640.

PT Reducing proliferation or extracellular matrix production by a cell in

PT liver and kidney, comprises administering a zveg4 antagonist -

PS Example 1; page 18-19; 34pp; English.

XX  
CC  
The present invention describes a method for reducing proliferation of

CC or extracellular matrix production by a cell in a mammal. The method comprises administering to the mammal a composition comprising a

CC therapeutically effective amount of a zvegi4 antagonist chosen from

zveg4 activation, and mitogenically inactive, receptor-binding variants

CC structurally related to platelet derived growth factor (PDGF) and

CC nephrotropic, hepatotropic, antiinflammatory, osteopathic and

CC of mesangial, epithelial, endothelial, smooth muscle, fibroblast,

CC in a mammal, in particular proliferation of prostate tumour cells, and osteoclast, neuronal, stromal, stellate or interstitial cells.

CC for reducing extracellular matrix production by a cell in a mammal  
CC suffering from a fibroproliferative disorder of kidney, bone or liver.

CC In particular it is useful for reducing stellate cell activation. The  
CC method is useful for reducing metastasis of prostate cancer cells to

CC bone in a mammal and for treating a fibroproliferative disorder of  
CC kidney, liver or bone in a mammal. Fibroproliferative disorders of the

CC kidney include, glomerulonephritis, diabetic glomerulosclerosis, lupus nephritis, renal arterioleclerosis and nephrotic syndrome disorders of

the liver include chronic active hepatitis and many other types of

CC osteosclerosis, osteoarthritis, and ectopic bone formation in metastatic

CC used in an example from the present invention.

SQ Sequence 1882 BP; 566 A; 407 C; 430 G; 479 T; 0 other;  
SQ

Query Match 1.3%; Score 377; DB 24; Length 1882;

Best Local Similarity 35.6%, Pled: NO. 4.4e-103,  
Matches 427: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

225 AAAAAAAAACTTTGATCTATATACACATAGACATGAATATATTTCTGTGTGTTGTGC 284

[illegible]

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QY 645 TAATACCT 652  
Db 1218 TAATACCT 1211

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Job time : 3758 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2003, 05:44:16 ; Search time 23547 Seconds  
(without alignments)  
20579.486 Million cell updates/sec

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Gapop 60.0 , Capext 60.0

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Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	652	2.2	3739	11 AF113216	AF113216 Homo sapi
C 2	572	1.9	606	14 BQ575044	BQ575044 UI-H-EZ1-
C 3	460	1.5	485	9 AA488996	AA488996 aa54cl0.s
C 4	431	1.4	482	9 AI799086	AI799086 we98b03.x
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C 6	337	1.1	407	9 AA748556	AA748556 oa57b11.s

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C 8	244	0.8	560	17	AW968905	AW968905 EST380981
C 9	241	0.8	926	17	BQ3230	BQ3230 CSRL-173C3-
C 10	197	0.7	248	9	AA491122	AA491122 aa46g03.r
C 11	187	0.6	452	17	AQ633340	AQ633340 RPCI-11-4
C 12	185	0.6	360	9	AA488780	AA488780 aa54cl0.f
C 13	163	0.5	406	9	AI221902	AI221902 q999h07.x
C 14	158	0.5	187	9	AA721242	AA721242 nz72c08.s
C 15	155	0.5	363	17	AQ111794	AQ111794 CIT-HSP-2
C 16	155	0.5	425	10	AW467833	AW467833 he26e05.x
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C 18	155	0.5	684	17	AG106397	AG106397 Pan trogl
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C 22	153	0.5	217	9	AI570720	AI570720 tr66a05.x
C 23	151	0.5	415	17	B43028	B43028 HS-1057-A1-
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C 37	144	0.5	640	9	AL157589	AL157589 DKFZp761H
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KEYWORDS	HTC					
SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 3739)					
AUTHORS	Liu, B., Liu, Y.O., Wang, X.Y., Zhao, B., Sheng, H., Zhang, X.W., Liu, S., Cao, H.Q., Zhao, Y., Liu, L.S., Ding, J.F., Gao, R.L., Wu, Q.Y., Qiang, B.Q., Yuan, J.G., Liew, C.C., Zhao, M.S. and Hui, R.T.					
TITLE	Submitted (15-DEC-1998) Molecular Medical Center for Cardiovascular Disease, Cardiovascular Institute, CAMS & PUMC, 167, Bei Li Shi Lu, Beijing 100037, P.R. China					
JOURNAL	Submitted (15-DEC-1998) Molecular Medical Center for Cardiovascular Disease, Cardiovascular Institute, CAMS & PUMC, 167, Bei Li Shi Lu, Beijing 100037, P.R. China					
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EAENDICRYDFEVEDISSTIIRGWCGRKEVPRIRKRNQIKIFKSDYFVAK
PGFKLYSLLEDQFQAAASSTWESYVSSISGVNSPVDPTLIADALDKKIAEFD
TVEDLLKIFNLESWEDLENMFLDTPRYRHSYHDKSKVDLDRINDAKRYSCPRN
YSVNIREEKLKLVVFFPRCLLVQRGCGNGCGTWNRSCTNSGKTVKKYHEVLOFE
PGHRRGRKATMALVLDIOLDHHCDCICSSRRPR"
BASE COUNT 1175 a 732 c 713 g 1119 t
ORIGIN

Query Match 2.2%; Score 652; DB 11; Length 3739;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATATGTAAAGAACCTCATCTTTTGATTTTAAATATACAAGATGCTTCTTTAAGAGA 60
DB 1743 GTATATGTAAAGAACCTCATCTTTTGATTTTAAATATACAAGATGCTTCTTTAAGAGA 1684

QY 61 GCAAGATTCAAAATGTTTGTGTTTCAAAATTTAAATAATTTATCTCTCTAAATTTT 120
DB 1683 GCAAGATTCAAAATGTTTGTGTTTCAAAATTTAAATAATTTATCTCTCTAAATTTT 1624

QY 121 CTAAGACATGTTTCATATATTGACCATCCCTTATTTGGCAAGAGATTTTAAGAGTCT 180
DB 1623 CTAAGACATGTTTCATATATTGACCATCCCTTATTTGGCAAGAGATTTTAAGAGTCT 1564

QY 181 AACTCAACATATGTAAAGCTCTGGTGACTCTGTTATATATACCAAAAAACATTTGAT 240
DB 1563 AACTCAACATATGTAAAGCTCTGGTGACTCTGTTATATATACCAAAAAACATTTGAT 1504

QY 241 CTATATACATAGACATGAATATATTTCTGTGTGTTTGTGCATATATACCTCAAC 300
DB 1503 CTATATACATAGACATGAATATATTTCTGTGTGTTTGTGCATATATACCTCAAC 1444

QY 301 ACTATATTAATGCAATCCTATATCTTAGGTATAGAGTTGATGATATACCTTCTAC 360
DB 1443 ACTATATTAATGCAATCCTATATCTTAGGTATAGAGTTGATGATATACCTTCTAC 1384

QY 361 TTGCCATGGCATTAACAAGCAAGCTGAGACTCAGCAACCACTTGTGTTCAATTCATG 420
DB 1383 TTGCCATGGCATTAACAAGCAAGCTGAGACTCAGCAACCACTTGTGTTCAATTCATG 1324

QY 421 CAGGTAGTAGTAAGTTGGTTGGTGGTAGGAAAAGGTTCTTATCTCACCTCCTTAA 480
DB 1323 CAGGTAGTAGTAAGTTGGTTGGTGGTAGGAAAAGGTTCTTATCTCACCTCCTTAA 1264

QY 481 ACTAAGGTCTCTTCAGGCTTAATGTAGGATGTGCACATCTCTATCGAGGTGGTCTT 540
DB 1263 ACTAAGGTCTCTTCAGGCTTAATGTAGGATGTGCACATCTCTATCGAGGTGGTCTT 1204

QY 541 GAGCTGCAGATACATACATCGTTTCATGGTGATCCAACTGGATGTCAACTAGAGCCATG 600
DB 1203 GAGCTGCAGATACATACATCGTTTCATGGTGATCCAACTGGATGTCAACTAGAGCCATG 1144

QY 601 GTCTTAGTCTACCCCTCCTCTGTATGTGGCAGGCTCAAACTGTAATACCT 652
DB 1143 GTCTTAGTCTACCCCTCCTCTGTATGTGGCAGGCTCAAACTGTAATACCT 1092

RESULT 2
BQ575044
LOCUS
DEFINITION
606 bp mRNA linear EST 19-JUN-2002
UI-H-E21-bbd-o-15-0-UI.s1 NCI-CCAP Ch2 Homo sapiens cDNA clone
UI-H-E21-bbd-o-15-0-UI 3', mRNA sequence.
ACCESSION BQ575044
VERSION BQ575044.1 GI:21478361
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1 (bases 1 to 606)
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```
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitellis/ Rush Presbyterian, Dept. of
Orthopaedics
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-24, >AT-rich#Low complexity 122-142,
>AT-rich#Low complexity 249-325, >(TA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=yes.
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/db_xref="taxon:9606"
/clone="UI-H-E21-bbd-o-15-0-UI"
/clone_lib="NCI-CCAP_Ch2"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/notes="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)
with a modified polylinker; Site 1: Ecor I; Site 2: Not I;
NCI-CCAP_Ch2 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma Grade II. The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an Ecor I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
TGATCACGCT.
TAG_LIB=UI-H-E21
TAG_TISSUE=grade-2-chondrosarcoma
TAG_SEQ=ATCTAATG"
BASE COUNT 188 a 97 c 97 g 224 t
ORIGIN

Query Match 1.9%; Score 572; DB 14; Length 606;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATATGTAAAGAACCTCATCTTTTGATTTTAAATATACAAGATGCTTCTTTAAGAGA 60
DB 35 GTATATGTAAAGAACCTCATCTTTTGATTTTAAATATACAAGATGCTTCTTTAAGAGA 94

QY 61 GCAAGATTCAAAATGTTTGTGTTTCAAAATTTAAATAATTTATCTCTCTAAATTTT 120
DB 95 GCAAGATTCAAAATGTTTGTGTTTCAAAATTTAAATAATTTATCTCTCTAAATTTT 154

QY 121 CTAAGACATGTTTCATATATTGACCATCCCTTATTTGGCAAGAGATTTTAAGAGTCT 180
DB 155 CTAAGACATGTTTCATATATTGACCATCCCTTATTTGGCAAGAGATTTTAAGAGTCT 214

QY 181 AACTCAACATATGTAAAGCTCTGGTGACTCTGTTATATATACCAAAAAACATTTGAT 240
DB 215 AACTCAACATATGTAAAGCTCTGGTGACTCTGTTATATATACCAAAAAACATTTGAT 274

QY 241 CTATATACATAGACATGAATATATTTCTGTGTGTTTGTGCATATATACCTCAAC 300
DB 275 CTATATACATAGACATGAATATATTTCTGTGTGTTTGTGCATATATACCTCAAC 334

QY 301 ACTATTATTAATGCAATCCTATATCTTAGGTATAGAGTTGATGATATACCTTCTAC 360
DB 1143 ACTATTATTAATGCAATCCTATATCTTAGGTATAGAGTTGATGATATACCTTCTAC 1143
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Db      335 ACTATTATTAAATGCAATCCTATATCTTTAGGTATAGAAAGTTGATGATATACCTTTCTAC 394
QY      361 TTGCCATGGCATTAAACAAAGCAAGCTGAGACTCAGCAACCACTTCTGTTTCATTGCGATTG 420
Db      395 TTGCCATGGCATTAAACAAAGCAAGCTGAGACTCAGCAACCACTTCTGTTTCATTGCGATTG 454
QY      421 CAGGCTAGTAGTAAGTTTGGTCTGCTGGTAGGAAAGGGTCTCTATCTCTCACCCCTCTTAA 480
Db      455 CAGGCTAGTAGTAAGTTTGGTCTGCTGGTAGGAAAGGGTCTCTATCTCTCACCCCTCTTAA 514
QY      481 ACTAAGAGTTCTTTCAGGCTTAATGTAAGGATGTCACATTCCTCTATCGAGGTGTCCTT 540
Db      515 ACTAAGAGTTCTTTCAGGCTTAATGTAAGGATGTCACATTCCTCTATCGAGGTGTCCTT 574
QY      541 GAGCTGCAGATACAATCACATCCTTCATGGTG 572
Db      575 GAGCTGCAGATACAATCACATCCTTCATGGTG 606

RESULT 3
LOCUS   AA488996
DEFINITION aa54c10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824754 3',
mRNA sequence.
ACCESSION AA488996
VERSION   AA488996.1 GI:2218598
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 485)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgaps@email.nih.gov
          Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
          Ph.D., Gerald Marti, M.D.
          CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
          Bonaldo, Ph.D.
          CDNA Library Arrayed by: Greg Lennon, Ph.D.
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          www.bio.llnl.gov/bbrp/image/image.html
          Seq primer: -41ml3 fwd. Er from Amersham
          High quality sequence stop: 465.
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         /clone="IMAGE:824754"
         /clone_lib="NCI_CGAP_GCB1"
         /tissue_type="germinal center B cell"
         /lab_host="DH10B"
         /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
         polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
         was prepared from human tonsillar cells enriched for
         germinal center B cells by flow sorting (CD20+, IgD-),
         provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
         (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
         primed with a Not I - oligo(dT) primer
         [5'-TGTACCATCTGAAGTGGGAGCGGCGCTCATTTTCTTTT-3'
         ]. Double-stranded cDNA was ligated to Eco RI adaptors
         (Pharmacia), digested with Not I and cloned into the Not I
         and Eco RI sites of the modified pT7T3 vector. Library
         went through one round of normalization, and was
         constructed by Bento Soares and M. Fatima Bonaldo."
         161 a 72 c 75 g 177 t

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Query Match      1.5%; Score 460; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTATATGTAGAAAGCCTCATCTTTTTCATTTTAAATATACAAAGATGCTTTCTTTTAAAGAGA 60
Db      26 GTATATGTAGAAAGCCTCATCTTTTTCATTTTAAATATACAAAGATGCTTTCTTTTAAAGAGA 85
QY      61 GCAAGATTCCAAATTCCTTTTGTGTTTCAAAATTTAAATAATTTATCTCTCTTAAATTTT 120
Db      86 GCAAGATTCCAAATTCCTTTTGTGTTTCAAAATTTAAATAATTTATCTCTCTTAAATTTT 145
QY      121 CTAAGACATGTTTTCATATATTGGACCATCCCTTATTTTGGCAAGAGATTTTAAAGAGTCT 180
Db      146 CTAAGACATGTTTTCATATATTGGACCATCCCTTATTTTGGCAAGAGATTTTAAAGAGTCT 205
QY      181 AACTCAACATATGTAAGCTCTGGTGTACCTGGTTATATATACCAAAAAAACAATTTGAT 240
Db      206 AACTCAACATATGTAAGCTCTGGTGTACCTGGTTATATATACCAAAAAAACAATTTGAT 265
QY      241 CTATATACATACATGACATGAATATATTCTGTCTGTGTTTGTGCATATATATAAACCCTCAAAAC 300
Db      266 CTATATACATACATGACATGAATATATTCTGTCTGTGTTTGTGCATATATATAAACCCTCAAAAC 325
QY      301 ACTATTATTAAATGCAATCCTATATTCTTTAGGTATAGAAAGTTGATGATATACCTTTCTAC 360
Db      326 ACTATTATTAAATGCAATCCTATATTCTTTAGGTATAGAAAGTTGATGATATACCTTTCTAC 385
QY      361 TTGCCATGGCATTAAACAAAGCAAGCTGAGACTCAGCAACCACTTGTGTTTCATTGCGATTG 420
Db      386 TTGCCATGGCATTAAACAAAGCAAGCTGAGACTCAGCAACCACTTGTGTTTCATTGCGATTG 445
QY      421 CAGGCTAGTAGTAAGTTTGGTCTGCTAGGAAAGGGTC 460
Db      446 CAGGCTAGTAGTAAGTTTGGTCTGCTAGGAAAGGGTC 485

RESULT 4
LOCUS   AI799066/c
DEFINITION we98b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2349101 3' similar to contains OFR.T1 OFR repetitive element
; mRNA sequence.
ACCESSION AI799066
VERSION   AI799066.1 GI:5364538
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 482)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgaps@email.nih.gov
          This clone is available royalty-free through LLNL; contact the
          IMAGE Consortium (info@image.llnl.gov) for further information.
          Insert Length: 825 Std Error: 0.00
          Seq primer: -400P from Gibco
          High quality sequence stop: 476.
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         /lab_host="DH10B"
         /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
         a modified polylinker; Site_1: Not I; Site_2: Eco RI;
         Equal amounts of plasmid DNA from three normalized
         libraries (fetal lung NbHL19W, testis NHT, and B-cell

```

NCI\_CCAP\_GCBL) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Ratlna Bonaldo.

BASE COUNT	121 a	122 c	89 g	149 t	1 others
ORIGIN					

Query Match	1.4%	Score	431	DB	9	Length	482
Best Local Similarity	99.8%	Pred. No.	0				
Matches	481	Conservative	0	Mismatches	1	Indels	0
Gaps	0						
QY	25345	AAAGACTGGCTAGCTTTATATAAGAAAAGAGAGGTTTAAATGGCCTCACAGTTATGCATTGCCCTGG	25404				
DB	482	AAAGACTGGGTAGTTTATAAAGAAAAGAGAGGTTTAAATGGCCTCACAGTTATGCATTGCCCTGG	423				
QY	25405	GAGGCCCTAAGGAAACTTACAATCATCTGGCAGAAAGCGCAAGGAAGCAAGGCACGCTCTTA	25464				
DB	422	GAGGCCCTAAGGAAACTTACAATCATCTGGCAGAAAGCGCAAGGAAGCAAGGCACGCTCTTA	363				
QY	25465	CATGTGGCAGGAGGAGAGCATGTGTGCACTGTAGGGAACTGCCCTTTATAAAATCA	25524				
DB	362	CATGTGGCAGGAGGAGAGCATGTGTGCACTGTAGGGAACTGCCCTTTATAAAATCA	303				
QY	25525	TCAGATCTTGTGCCACTCACTCACTATCNCAGAAATAGCATGGGGAAACCATCCCAATG	25584				
DB	302	TCAGATCTTGTGCCACTCACTCACTATCACAAGAAATAGCATGGGGAAACCATCNCATG	243				
QY	25585	ATTCAATTAATCTCCATCTTGTTCCTCCCTTGACATGTGGGGATTATGGGGAATTATGGGGA	25644				
DB	242	ATTCAATTAATCTCCATCTTGTTCCTCCCTTGACATGTGGGGATTATGGGGAATTATGGGGA	183				
QY	25645	TTGCAATTCAAGATGAGATTTTGGGTGGGACACAATGCATACTATATTAGCAAGTAAAG	25704				
DB	182	TTGCAATTCAAGATGAGATTTTGGGTGGGACACAATGCATACTATATTAGCAAGTAAAG	123				
QY	25705	ACACTCAGTGTGGATCTCTCAGCACCCAGCAGGGCCCTACAGCATATATGCTCTTAGGA	25764				
DB	122	ACACTCAGTGTGGATCTCTCAGCACCCAGCAGGGCCCTACAGCATATATGCTCTTAGGA	63				
QY	25765	GCAGTGTAGTGTCTCCTTTAAGTCTAGTGGGGCATAAAGGAAACCAATCCCATATAATTT	25824				
DB	62	GCAGTGTAGTGTCTCCTTTAAGTCTAGTGGGGCATTAAGGAAACCAATCCCATATAATTT	3				
QY	25825	TC	25826				
DB	2	TC	1				

RESULT 5	AW977062	LOCUS	AW977062	582 bp	linear	EST 02-JUN-2000
DEFINITION	EST389171	MAGE resequences,	MAGO Homo sapiens	cdNA,		mRNA sequence.
ACCESSION	AW977062					
KEYWORDS	AW977062.1	GI:8168303				
SOURCE	EST.		human.			
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	1 (bases 1 to 582) Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, J. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and Quackenbush, J.					
TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray					
JOURNAL	Unpublished (2000)					
COMMENT	Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA					

```

Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 371
Seq primer: Forward.
Location/Qualifiers
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    /db_xref="taxon:9606"
    /clone_lib="MAGE resources, MAGO"
    /note="Vector: pBluescriptSKm"
BASE COUNT    163 a    118 c    100 q    201 t

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Query Match	1.2%	Score 367;	DB 10;	Length 582;
Best Local Similarity	99.8%;	Pred. No. 0;		
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QY	17306	TATTTTGCCTATCTTTTATTGTGCGCAAAATTTATTAAATGATATATAATTGAATTAAGGTTTTCG	17365	
Db	1	TATTTTGCTATCTTTTATTGTGCGCAAAATTTATTAAATGATATATAATTGAATTAAGGTTTTCG	60	
QY	17366	TTATGAGATTGTGCGCGTCATATCCCTGTAATGAATTAACATCATATTTCTCTTTTTTCTGT	17425	
Db	61	TTATGAGATTGTGCGCGTCATATCCCTGTAATGAATTAACATCATATTTCTCTTTTTTCTGT	120	
QY	17426	TCCTTTTCCGAAGTAGGTCGAAGCTCTGAAATTTACTGTATCACATATTTTGCAATATATATCT	17485	
Db	121	TCCTTTTCCGAAGTAGGTCGAAGCTCTGAAATTTACTGTATCACATATTTTGCAATATATATCT	180	
QY	17486	AACAATGTTGATGTTTGATCCACATGGTGTATTGTTCAAATTTAGAAAAACAGTCGCTTCG	17545	
Db	181	AACAATGTTGATGTTTGATCCACATGGTGTATTGTTCAAATTTAGAAAAACAGTCGCTTCG	240	
QY	17546	TCAGGATAGGATTAACCTTGTCATCAGGACACTTGGCTTGGCAAACTAGTGTGGGTAGAA	17605	
Db	241	TCAGGATAGGATTAACCTTGTCATCAGGACACTTGGCTTGGCAAACTAGTGTGGGTAGAA	300	
QY	17606	TTTCTGCTTCTTAATCAAAACCTTGGCTGGTGCCCTTGTGCGAGTGGAACAACCTGAACAACT	17665	
Db	301	TTTCTGCTTCTTAATCAAAACCTTGGCTGGTGCCCTTGTGCGAGTGGAACAACCTGAACAACT	360	
QY	17666	GTATGCAATGGCCCTGTCTTCTGTAATCCTATAGATTAAAGCATTTGCAACAAGAATCT	17723	
Db	361	GTATGCAATGGCCCTGTCTTCTGTAATCCTATAGATTAAAGCATTTGCAACAAGAATCT	418	

RESULT 6	AA748556	407 bp	mrna	linear	EST 27-JAN-1998
LOCUS	AA748556				
DEFINITION	AA748556.1 NCICGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309053 3', mrna sequence.				
ACCESSION	AA748556				
VERSION	AA748556.1	GI:2788514			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 407)				
AUTHORS	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .				
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
JOURNAL	Unpublished (1997)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a> Tissue Procurement: Louis M. Staudt, M.D., David Allman, Ph.D., Gerald Marti, M.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be				

found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/brp/image/image.html  
Insert Length: 1291 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 389.  
Location/Qualifiers

FEATURES  
source

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/lab\_host="DH10B"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from human tonsillar cells enriched for  
germinal center B cells by flow sorting (CD20+, IgD-),  
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman  
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was  
primed with a Not I - oligo(dT) primer  
[5'-TGTACCAATCGAAGTGGAGCGCGCTCATTTTCTTTT-3',  
Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT7T3 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 108 a 72 c 71 g 156 t  
ORIGIN

Query Match 1.1%; Score 337; DB 9; Length 407;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 387; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 17302 TTTATATTTCGCTATCTTTATTCGCGCAATTTTAAATGATATATTCGAATTAAGGTT 17361  
Db 14 TTTATATTTCGCTATCTTTATTCGCGCAATTTTAAATGATATATTCGAATTAAGGTT 73  
QY 17362 TTGCTTATGAGATTGTGCGCTCATATCTCTGTAATGAATTAACATCATATATTCCTCTTTT 17421  
Db 74 TTGCTTATGAGATTGTGCGCTCATATCTCTGTAATGAATTAACATCATATATTCCTCTTTT 133  
QY 17422 TCTGCTTTCTGCAAGTAGTCAAGCTCGAATTTACTGTATACATATTTGATATATA 17481  
Db 134 TCTGCTTTCTGCAAGTAGTCAAGCTCGAATTTACTGTATACATATTTGATATATA 193  
QY 17482 TTCTAAATGTTGATGTTGATCCACATGCTGATGTTTCAAAATAGAAAAACAGTGCC 17541  
Db 194 TTCTAAATGTTGATGTTGATCCACATGCTGATGTTTCAAAATAGAAAAACAGTGCC 253  
QY 17542 TTGCTCAGATAGATTAACTGTCTATCAGGACACTTGGCTTGGCAAACTAGTGTGGGT 17601  
Db 254 TTGCTCAGATAGATTAACTGTCTATCAGGACACTTGGCTTGGCAAACTAGTGTGGGT 313  
QY 17602 AGAATTTCTGCTCTTAATCAAACTGGCGGTGGCTTGTGCAGTGAACACCTGAAC 17661  
Db 314 AGAATTTCTGCTCTTAATCAAACTGGCGGTGGCTTGTGCAGTGAACACCTGAAC 373  
QY 17662 AACTGTATGCAATGGCCCTGCTCTCTG 17689  
Db 374 AACTGTATGCAATGGCCCTGCTCTCTG 401

RESULT 7  
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LOCUS  
DEFINITION xn34502.x1 NCI\_CGAP\_Kid11 Homo sapiens cDNA clone IMAGE:2695563 3',  
mRNA sequence.  
ACCESSION AW274723  
VERSION AW274723.1 GI:6661753  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 505)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/brp/image/image.html  
Seq primer: -40UP from Gibco  
High quality sequence stop: 475.  
Location/Qualifiers

FEATURES  
source

1. .505  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2695563"  
/clone\_lib="NCI\_CGAP\_Kid11"  
/lab\_host="DH10B"  
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with  
a modified polylinker; Site 1: Not I; Site 2: Eco RI;  
Plasmid DNA from the normalized library NCI\_CGAP\_Kid3 was  
prepared, and ss circles were made in vitro. Following HAP  
purification, this DNA was used as tracer in a subtractive  
hybridization reaction. The driver was PCR-amplified cDNAs  
from a pool of 5,000 clones made from the same library  
(cloneIDs 1322376-1323911, 1456007-1456775, and  
1500552-1502855). Subtraction by Bento Soares and M.  
Fatima Bonaldo."  
BASE COUNT 169 a 83 c 75 g 178 t  
ORIGIN

Query Match 0.9%; Score 263; DB 10; Length 505;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 225 AAAAAAACATTTGATCTATATACATAGACATGAATATTTCTGTGTGTTGTC 284  
Db 243 AAAAAAACATTTGATCTATATACATAGACATGAATATTTCTGTGTGTTGTC 302  
QY 285 ATATATAACCTCAAACTATATTAATGCAATCTTATTTCTTAGGTATAGAAGTTGA 344  
Db 303 ATATATAACCTCAAACTATATTAATGCAATCTTATTTCTTAGGTATAGAAGTTGA 362  
QY 345 TGATATACCTTTCTACTTGGCATTAACAAAGCAAGCTGAGACTCAGCAACCACT 404  
Db 363 TGATATACCTTTCTACTTGGCATTAACAAAGCAAGCTGAGACTCAGCAACCACT 422  
QY 405 TGTGTTTCATTCGCTTGCAGGCTAGTAGTAAGTTGGTTGGTTAGGAAAAGGTCCTCTT 464  
Db 423 TGTGTTTCATTCGCTTGCAGGCTAGTAGTAAGTTGGTTGGTTAGGAAAAGGTCCTCTT 482  
QY 465 ATCTCACCCCTCTTAAACTAAAG 487  
Db 483 ATCTCACCCCTCTTAAACTAAAG 505

RESULT 8  
AW968905/c  
LOCUS  
DEFINITION AW968905  
ACCESSION AW968905  
VERSION AW968905.1 GI:8158746  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 560)  
 AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.  
 TITLE Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: John Quackenbush  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 3528  
 Fax: 301 838 0208  
 Email: johnq@tigr.org  
 Plate: 258  
 Seq primer: Forward.  
 Location/Qualifiers  
 l..560  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="MAGE resequences, MAGJ"  
 /note="Vector: pBluescriptSKm"

BASE COUNT 163 a 122 c 120 g 155 t  
 ORIGIN  
 Query Match 0.8%; Score 244; DB 10; Length 560;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 358 TACTTGGCCATGATTAACAAGCAAGGCTGAGACTCAGCACCACTGTGTTCATTGCA 417  
 DB 411 TACTTGGCCATGATTAACAAGCAAGGCTGAGACTCAGCACCACTGTGTTCATTGCA 352  
 QY 418 TTGCAGGCTAGTAGTAAGTTTGGTTGCTGGTAGGAAAGGGTCTTATCTCACCTCT 477  
 DB 351 TTGCAGGCTAGTAGTAAGTTTGGTTGCTGGTAGGAAAGGGTCTTATCTCACCTCT 292  
 QY 478 TAACTAAAGGTTCTTTTTCAGGCTTAATGTAAGGATGTGCACATTCCTTATCGAGGTGGT 537  
 DB 291 TAACTAAAGGTTCTTTTTCAGGCTTAATGTAAGGATGTGCACATTCCTTATCGAGGTGGT 232  
 QY 538 CTTGAGCTGCAGATACATACATCATGTTTCATGGTATCCAACTGGATGCACTAGAGCC 597  
 DB 231 CTTGAGCTGCAGATACATACATCATGTTTCATGGTATCCAACTGGATGCACTAGAGCC 172  
 QY 598 ATGGTCTTAGCTCTACCCCTCTCTTGATGTGGCCAGGCTCAAACTGTAATACCT 652  
 DB 171 ATGGTCTTAGCTCTACCCCTCTCTTGATGTGGCCAGGCTCAAACTGTAATACCT 117

RESULT 9  
 B03230/c  
 LOCUS B03230 926 bp DNA linear GSS 13-JUL-1996  
 DEFINITION CSRL-173C3-u CSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone CSRL-173C3, DNA sequence.  
 ACCESSION B03230  
 VERSION B03230.1 GI:1412508  
 KEYWORDS GSS.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 926)  
 REFERENCE Jones,G.A., Burbee,D., Davies,C., Hahner,L., Oliver,T., Gilbert,M., Evans,D., Ward,T., Gillilan,E., Schagemann,J., Probst,S., Harris,J., DeFord,J., McFarland,J., Burzinski,K., Khan,M., Kupfer,K. and Garner,H.R.  
 TITLE Genomic Sequence Sampled Map of Chromosome 11  
 JOURNAL Unpublished (1996)  
 COMMENT Contact: Evans GA, Shane Probst  
 McDermott Center for Human Growth and Development  
 University of Texas Southwestern Medical Center At Dallas  
 5323 Harry Hines Blvd, Dallas TX 75235-8591

Tel: 214-648-1600  
 Fax: 214-648-1666  
 Email: gevans@utsw.swmed.edu, shane@mcdermott.swmed.edu  
 PCR PRIMERS  
 FORWARD: TGGTTTGTAGAGTGGAGCTTG  
 BACKWARD: ACAATGTTTATTGGGATG  
 Seq primer: T7  
 Class: cosmid ends  
 High quality sequence stop: 926.  
 Location/Qualifiers  
 l..926  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="CSRL-173C3"  
 /clone\_lib="CSRL flow sorted Chromosome 11 specific cosmid"  
 /sex="female"  
 /cell\_type="chimeric hamster somatic cell hybrid"  
 /note="Vector: sCos-1; Human Chromosome 11 specific cosmid library prepared from flow sorted human Chromosome 11 derived from Chinese Hamster Ovary (CHO) monochromosomal somatic cell hybrid, J1"

BASE COUNT 313 a 185 c 136 g 254 t 38 others  
 ORIGIN  
 Query Match 0.8%; Score 241; DB 17; Length 926;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 291; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23333 TATTCAGGTGCTCTCTTCTTATTTGAACATAAAAAAGTTGTTGGAGTAGAGACTAATCAT 23392  
 DB 363 TATTCAGGTGCTCTCTTCTTATTTGAACATAAAAAAGTTGTTGGAGTAGAGACTAATCAT 304  
 QY 23393 CTTTTTATCCCTTCTTCTTCTAGTACTTTGTCCTTAATGTAAGGACCAATGCGCTCAT 23452  
 DB 303 CTTTTTATCCNTTCTTCTTCTAGTACTTTGTCCTTAATGTAAGGACCAATGCGCTCAT 244  
 QY 23453 CAAGCTCACTTCTTAAACCACTTTGACTTCAACGATTAGGAGCAAGGTGCTGCTGAAGGAA 23512  
 DB 243 CAAGCTCACTTCTTAAACCACTTTGACTTCAACGATTAGGAGCAAGGTGCTGCTGAAGGAA 184  
 QY 23513 GCACAACTGCTCTTTGTCGAGATTCCTTTGCAAGAAATAGACACTCAATAATTACTA 23572  
 DB 183 GCACAACTGCTCTTTGTCGAGATTCCTTTGCAAGAAATAGACACTCAATAATTACTA 124  
 QY 23573 CCTGAATGAATCAGATAAACACATGATTTTTCAGTTAATTTTATCACA 23624  
 DB 123 CCTGAATGAATCAGATAAACACATGATTTTTCAGTTAATTTTATCACA 72

RESULT 10  
 AA491122/c  
 LOCUS AA491122 248 bp mRNA linear EST 18-AUG-1997  
 DEFINITION aa4903.r1 NCL\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:824020 5', mRNA sequence.  
 ACCESSION AA491122  
 VERSION AA491122.1 GI:2220295  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 248)  
 REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 TITLE Unpublished (1997)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgapsb@mail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.



cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/dbp/image/image.html](http://www-bio.llnl.gov/dbp/image/image.html)  
 Seq primer: -28ml3 revl Et from Amersham  
 High quality sequence stop: 141.  
 Location/Qualifiers

# FEATURES

1. 248  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="824020"  
 /clone\_lib="NCI-CGAP\_GCB1"  
 /tissue\_type="germinal center B cell"  
 /lab\_host="DH10B"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
 was prepared from human tonsillar cells enriched for  
 germinal center B cells by flow sorting (CD20+, IgD-),  
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman  
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was  
 primed with a Not I - oligo(dT) primer  
 [5'-TGTTACCAATCTGAAGTGGAGGGCGGCTCATTTTTTTTTTTT-3'  
 ]. Double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT73 vector. Library  
 went through one round of normalization, and was  
 constructed by Bento Soares and M. Fatima Bonaldo."  
 75 a 56 c 42 g 75 t

BASE COUNT  
 ORIGIN

Query Match 0.7%; Score 197; DB 9; Length 248;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 247; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 14542 TGACACATCTCAAGGATATTCAGGAGTCTCAGGGGCATATGACAGGAGTGTGTTTCCA 14601  
 DB 248 TGACACATCTCAAGGATATTCAGGAGTCTCAGGGGCATATGACAGGAGTGTGTTTCCA 189  
 QY 14602 GGTAGCAGTACTGCGTGGTGATGGATGTTTATTTTCCCTTCATCCAGCACATGACAG 14661  
 DB 188 GGTAGCAGTACTGCGTGGTGATGGATGTTTATTTTCCCTTCATCCAGCACATGACAG 129  
 QY 14662 AGTGATTTATAGAGCTTTGACAGAGTCTAGAAAGTAAATATTAGGACACATGCTTAA 14721  
 DB 128 AGTGATTTATAGAGCTTTGACAGAGTCTAGAGTAAATATTAGGACACATGCTTAA 69  
 QY 14722 AGAGATGCTTTAGATACAGTTTCAAGGATGCGCAATGTTTCAATPCCACTCATCGGACTG 14781  
 DB 68 AGAGATGCTTTAGATACAGTTTCAAGGATGCGCAATGTTTCAATPCCACTCATCGGACTG 9  
 QY 14782 AACAAAGA 14789  
 DB 8 AACAAAGA 1

RESULT 11  
 A0633340/c  
 LOCUS  
 DEFINITION  
 A0633340  
 VERSION  
 A0633340.1 GI:5095975  
 KEYWORDS  
 GSS.  
 SOURCE  
 human.  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 1 (bases 1 to 452)  
 AUTHORS  
 Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter  
 ,J.C.  
 TITLE  
 use of BAC End Sequences from Library RPCI-11 for Sequence-Ready  
 Map Building

# JOURNAL COMMENT

Unpublished (1997)  
 Other\_GSSs: RPCI-11-475J2.TV  
 Contact: Shaying Zhao, William Nierman, Mark Adams  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: hbe@tigr.org  
 Clones are derived from the human BAC library RPCI-11. For BAC  
 library availability, please contact Pieter de Jong  
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from  
 BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from  
 Research Genet cs ([infoceresgen.com](http://infoceresgen.com)). BAC end search page:  
[http://www.tigr.org/tdb/humgen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html).  
 Seq primer: SP6  
 Class: BAC ends.

# FEATURES

Location/Qualifiers  
 1. 452  
 /organism="Homo sapiens"  
 /db\_xref="GDB:7682233"  
 /db\_xref="taxon:9606"  
 /clone="RPCI-11-475J2"  
 /clone\_lib="RPCI-11"  
 /sex="Male"  
 /cell\_type="Lymphocytes"  
 /note="Vector: pBACE3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
 RPCI11 Human Male BAC Library"  
 159 a 76 c 82 g 132 t 3 others

BASE COUNT  
 ORIGIN

Query Match 0.6%; Score 187; DB 17; Length 452;  
 Best Local Similarity 99.3%; Pred. No. 0;  
 Matches 287; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 18435 AATGTAATAAGAAAAGGGTTTTAGTTTTATTTTAACTTCAAAAGTTAATCAACATGTTA 18494  
 DB 404 AATGTAATAAGAAAAGGGTTTTAGTTTTATTTTAACTTCAAAAGTTAATCAACATGTTA 345  
 QY 18495 GAGAAATGATTTTTTGTGTGTAATATGTTGATGATATTTGTCACCTGGGTCCTAGATGG 18554  
 DB 344 GAGAAATGATTTTTTGTGTGTAATATGTTGATGATATTTGTCACCTGGGTCCTAGATGG 285  
 QY 18555 CAGTATACATAGTGGTTTAACTGCTTTGGAGCCGAGTAAAGTTACAACTGCCTTCAATC 18614  
 DB 284 CAGTATACATAGTGGTTTAACTGCTTTGGAGCCGAGTAAAGTTACAACTGCCTTCAATC 225  
 QY 18615 ACATCATGGCTATGTTTCCCTTTTATGTTGGAAGTTATTTAATAGGCTCTGAACCTTCTGCTT 18674  
 DB 224 ACATCATGGCTATGTTTCCCTTTTATGTTGGAAGTTATTTAATAGGCTCTGAACCTTCTGCTT 165  
 QY 18675 CCTCATCTATACATGTAATCAATTTGAAGATTTGAATTAAGTAACTGACCTG 18723  
 DB 164 CCTCATCTATACATGTAATCAATTTGAAGATTTGAATTAAGTAACTGACCTG 116

RESULT 12  
 AA488780/c  
 LOCUS  
 DEFINITION  
 aa54c10.r1 NCI-CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:824754 5',  
 mRNA sequence.  
 ACCESSION  
 AA488780  
 VERSION  
 AA488780.1 GI:2218382  
 KEYWORDS  
 EST.  
 SOURCE  
 human.  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 1 (bases 1 to 360)  
 AUTHORS  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 JOURNAL

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html  
Seq primer: -28m13 rev1 Er from Amersham  
High quality sequence stop: 358.

## FEATURES

source

1. .360  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:824754"  
/clone\_lib="NCI-CGAP\_GCB1"  
/tissue\_type="germinal center B cell"  
/lab\_host="DH10B"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer  
[5'-TGTTACCATCTCAAGTGGGAGCGCGCTCATTTTCTTTT-3'  
]. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

108 a 77 c 86 g 89 t

Query Match

Best Local Similarity 0.6%; Score 185; DB 9; Length 360;

Matches 285; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

366 ATGCATTACAAAGCAGGCTGAGACTCAGCAACCACTTGTGTTTCATTCGATGAGGC 425

Db

360 ATGCATTACAAAGCAGGCTGAGACTCAGCAACCACTTGTGTTTCATTCGATGAGGC 301

QY

426 TAGTAGTAAGTGTGGTGGTAGGAAAGGGTCTTATCTCACCCCTCTTAAACTAA 485

Db

300 TAGTAGTAAGTGTGGTGGTAGGAAAGGGTCTTATCTCACCCCTCTTAAACTAA 241

QY

486 AGGTTCTTTCAGGCTTAATGAAGGATGTCACATTCCTTATCGAGGTGGTCTTGAGCT 545

Db

240 TGGTCTTCTCAGGCTTAATGAAGGATGTCACATTCCTTATCGAGGTGGTCTTGAGCT 181

QY

546 GCAGATCAATCATCGTTTCATGGTGATCCCACTGATGTCACATGATGAGCCATGCTTT 605

Db

180 GCAGATCAATCATCGTTTCATGGTGATCCCACTGATGTCACATGATGAGCCATGCTTT 121

QY

606 AGCTTACCCCTCTCTTGTATGGCCAGGCTCAAACTGTAATACCT 652

Db

120 AGCTTACCCCTCTCTTGTATGGCCAGGCTCAAACTGTAATACCT 74

RESULT 13

AI221902

LOCUS

DEFINITION

GG99h07.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone

IMAGE:1843357.3', mRNA sequence.

ACCESSION

AI221902

VERSION

AI221902.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 406)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
This clone is available royalty-free through LLNL; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Insert length: 902 Std Error: 0.00  
Seq primer: -400P from Gibco  
High quality sequence stop: 394.

## FEATURES

source

1. .406  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1843357"  
/clone\_lib="Soares\_NFL\_T\_GBC\_S1"  
/lab\_host="DH10B"  
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI-CGAP\_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

146 a 62 c 52 g 146 t

Query Match

Best Local Similarity 0.5%; Score 163; DB 9; Length 406;

Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

225 AAAAAAACATTTGATCTATATACATACATAGACATATATTTCTGTGTGTTGTGC 284

Db

244 AAAAAAACATTTGATCTATATACATACATAGACATATATTTCTGTGTGTTGTGC 303

QY

285 ATATATAACCTCAAAACACTATTATTAATGCAATCCTATATTTCTAGGTATAGAAGTTGA 344

Db

304 ATATATAACCTCAAAACACTATTATTAATGCAATCCTATATTTCTAGGTATAGAAGTTGA 363

QY

345 TGATATACCTTTCTACTTGGCATGGAATTAACAAGCAAGGCT 387

Db

364 TGATATACCTTTCTACTTGGCATGGAATTAACAAGCAAGGCT 406

RESULT 14

AA721242

LOCUS

DEFINITION

n272c08.s1 NCI-CGAP\_GCB1 Homo sapiens cDNA clone

IMAGE:1301006.3', mRNA sequence.

ACCESSION

AA721242

VERSION

AA721242.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 187)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., David Allman, Ph.D., Gerald Marti, M.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone Distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
 Insert Length: 1250 Std Error: 0.00  
 Seq primer: -40ml3 fwd. RT from Amersham  
 High quality sequence stop: 65.

# FEATURES

source  
 1. .187  
 /organism="Homo sapiens"  
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 /clone="IMAGE:1301006"  
 /clone\_lib="NCI-CCAP\_GCB1"  
 /tissue\_type="germinal center B cell"  
 /lab\_host="DH10B"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+ IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTACCAATCTCAAGTGGGAGCGCGCTCATTTTTTTTTTT-3' (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo." 49 a 24 c 23 g 91 t

Query Match 0.5%; Score 158; DB 9; Length 187;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17302 TTTATATTTGCTATCTTTATTGCGCAATTTTAAATGATATATTAAGTT 17361  
 Db 14 TTTATATTTGCTATCTTTATTGCGCAATTTTAAATGATATATTAAGTT 73

Qy 17362 TTGCTTATGAGATGTGCGGTATATCTCTAAATGAATACATCATATTCTTTT 17421  
 Db 74 TTGCTTATGAGATGTGCGGTATATCTCTAAATGAATACATCATATTCTTTT 133

Qy 17422 TCCTCTTTCTGCAAGTAGTCAAGCTCTCAATTA 17459  
 Db 134 TCCTCTTTCTGCAAGTAGTCAAGCTCTCAATTA 171

# RESULT 15

AQ111794/c  
 LOCUS AQ111794 363 bp DNA linear GSS 29-AUG-1998  
 DEFINITION CIT-HSP-2379H19.TF CIT-HSP Homo sapiens genomic clone 2379H19, DNA sequence.  
 ACCESSION AQ111794  
 VERSION AQ111794.1 GI:3488451  
 KEYWORDS GSS.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 363)  
 AUTHORS Adams,M.D.; Rounsley,S.D.; Zhao,S.; Bass,S.; Linher,K.; Golden,K.; Berry,K.; Granger,D.; Suh,E.; Wible,C.; Shizuya,H.; Simon,M. and Venter,J.C.  
 TITLE Use of a random human BAC End Sequence Database for Sequence-Ready Map Building  
 JOURNAL Unpublished (1998)  
 COMMENT Other\_GSSs: CIT-HSP-2379H19.TR  
 Contact: Mark Adams  
 Department of Eukaryotic Genomics

The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: [mdadams@tigr.org](mailto:mdadams@tigr.org)  
 Clones are available from Research Genetics ([info@resgen.com](mailto:info@resgen.com)). BAC end search page:  
[http://www.tigr.org/tcdb/hungen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tcdb/hungen/bac_end_search/bac_end_search.html).  
 Seq primer: M13-21  
 Class: BAC ends.

# FEATURES

source  
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 /clone="2379H19"  
 /clone\_lib="CIT-HSP"  
 /sex="Male"  
 /cell\_type="Sperm"  
 /note="Vector: pBelobAC11; Site\_1: HindIII; Site\_2: HindIII"  
 142 a 83 c 65 g 73 t

Query Match 0.5%; Score 155; DB 17; Length 363;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29325 GTTGCCTGTTCACTCTCATGCTAGTCTTTTCTGCTGCGAGAGCTCTTTAGTTAATTA 29384  
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Qy 29385 GATCCCATTTGTCAATTTTGGCTTTTGTGCCATTTGCTTTGGTGTGTTTGTAGACATGAAGT 29444  
 Db 288 GATCCCATTTGTCAATTTTGGCTTTTGTGCCATTTGCTTTGGTGTGTTTGTAGACATGAAGT 229

Qy 29445 CCTTGGCCATGCGCTATGCTCTGAATGCTATGCTT 29479  
 Db 228 CCTTGGCCATGCGCTATGCTCTGAATGCTATGCTT 194

Search completed: July 8, 2003, 03:58:37  
 Job time : 23556 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2003, 05:16:49 ; Search time 48544 Seconds  
(without alignments)  
17938.057 Million cell updates/sec

Database: us-10-083-853b-2

Sequence: 1 gtagatgtaagaagcctca.....caattctgtgaagaagtaa 29921

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: GenBank

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3: gb.in.\*

4: gb.ov.\*

5: gb.pat.\*

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14: em.ba.\*

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44: em.htgo\_man.\*

45: em.htgo\_vrt.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26958	90.1	182403	2	AC024052 Homo sapi
2	23856	79.7	180648	2	AP003043 Homo sapi
3	5698	19.6	160345	2	AC067870 Homo sapi
4	5610	19.7	160345	2	AC067870 Homo sapi
5	762	2.5	1149	9	AK025378 Homo sapi
6	652	2.2	1587	6	AX164746 Sequence
7	652	2.2	1734	6	AX164761 Sequence
8	652	2.2	1828	6	AX164744 Sequence
9	652	2.2	1828	9	AF335584 Homo sapi
10	652	2.2	3718	6	AX365307 Sequence
11	652	2.2	3736	6	AX365305 Sequence
12	652	2.2	4070	9	BC030645 Homo sapi
13	601	2.0	2253	9	AF336376 Homo sapi
14	550	1.8	3710	9	AY027518 Homo sapi
15	550	1.8	3729	9	AY027517 Homo sapi
16	460	1.5	485	6	AX331460 Sequence
17	377	1.3	1882	6	AX044487 Sequence
18	377	1.3	1882	6	AX207483 Sequence
19	236	0.8	1428	9	AB033832 Homo sapi
20	221	0.7	1162	6	AX454728 Sequence
21	221	0.7	1162	6	AX464052 Sequence
22	221	0.7	1162	6	AX491206 Sequence
23	221	0.7	1404	6	AX365309 Sequence
24	221	0.7	1404	6	AX463715 Sequence
25	220	0.7	462	6	AX164752 Sequence
26	220	0.7	199386	9	AC117440 Homo sapi
27	220	0.7	228137	2	AC117483 Homo sapi
28	190	0.6	173386	9	AC084781 Homo sapi
29	190	0.6	209779	9	AC066616 Homo sapi
30	185	0.6	156633	2	AC113431 Homo sapi
31	174	0.6	193404	2	AC103693 Homo sapi
32	174	0.6	213564	2	AC091030 Homo sapi
33	173	0.6	81374	9	HSJ300H18
34	172	0.6	3337	9	HSJ18142
35	172	0.6	3512	9	HSAC001014
36	172	0.6	3512	9	HUM43DC97Z
37	172	0.6	76819	9	AC004043 Homo sapi
38	172	0.6	83072	9	AL356793 Human DNA
39	172	0.6	116685	9	HS516C23
40	172	0.6	168936	2	AC024992 Homo sapi
41	172	0.6	198586	9	AC079789 Homo sapi
42	170	0.6	170289	9	AC097648 Homo sapi
43	169	0.6	136495	9	AC005521 Homo sapi
44	168	0.6	3060	9	AB013905 Homo sapi
45	168	0.6	6091	9	HSDBRPE

ALIGNMENTS

RESULT 1  
AC024052

LOCUS  
DEFINITION

AC024052  
Homo sapiens chromosome 11 clone RP11-617B3, WORKING DRAFT

AC024052  
SEQUENCE, 7 unordered pieces.

AC024052.3  
HTG; HTGS\_PHASE1; HTGS\_DRAFT

HTG; HTGS\_PHASE1; HTGS\_DRAFT  
Homo sapiens

ORGANISM  
Homo sapiens

REFERENCE  
1 (bases 1 to 182403)

AUTHORS  
Waterston,R.H.

TITLE  
The sequence of Homo sapiens clone

AC024052 182403 bp DNA linear HTG 17-AUG-2000  
Homo sapiens chromosome 11 clone RP11-617B3, WORKING DRAFT

SEQUENCE, 7 unordered pieces.

AC024052.3 GI:9838295  
HTG; HTGS\_PHASE1; HTGS\_DRAFT

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 182403)

Waterston,R.H.

The sequence of Homo sapiens clone

Pred. No. is the number of results predicted by chance to have a

JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Unpublished  
2 (bases 1 to 182403)  
Waterston,R.H.  
Direct Submission  
Submitted (20-FEB-2000) Genome Sequencing Center, Washington  
University School of Medicine, 444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
On Aug 17, 2000 this sequence version replaced gi:7109658.

## COMMENT

----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu/gsc/index.shtml>  
----- Project Information -----  
Center project name: H.NH0617B03  
----- Summary Statistics -----  
Sequencing vector: M13; 100%  
Sequencing vector: plasmid; 0%  
Chemistry: Dye-primer ET; 100% of reads  
Chemistry: Dye-terminator Big Dye; 0% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 178574 bases at least Q40  
Consensus quality: 179480 bases at least Q30  
Consensus quality: 179940 bases at least Q20  
Insert size: 198000; agarose-fp  
Quality coverage: 5.39 in Q20 bases; agarose-fp  
Quality coverage: 5.87 in Q20 bases; sum-of-contigs  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 7 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence.  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1666: contig of 1666 bp in length  
1667 1766: gap of unknown length  
1767 9133: contig of 7367 bp in length  
9133 9233: gap of unknown length  
9233 20663: contig of 11430 bp in length  
20663 20763: gap of unknown length  
20763 35927: contig of 15164 bp in length  
35927 36028: gap of unknown length  
36028 61610: contig of 25583 bp in length  
61610 61710: gap of unknown length  
61710 96167: contig of 34457 bp in length  
96167 96267: gap of unknown length  
96267 182403: contig of 86136 bp in length.

## FEATURES

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/chromosome="11"  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 29921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 136115 GTATATGTAAGAAAGCCATCTTTTGGATTTTAAATATACAAGATGCTTCTTTTAAGAGA 136174  
QY 61 GCAAGATTCAAAATTTGTTTGTGTTTCAAAATTTAAATTTATATCTCCTAAATTTT 120  
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Qy 2041 GCACAGATTTGAGCTCTGATAGGGACAGGCTGCCCTCCTCAAGTGGGTCCCTGACCCCC 2100  
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Db 138155 GCACAGATTTGAGCTCTGATAGGAGAGAGCTGCCCTCCTCAAGTGGGTCCCTGACCCCC 138214  
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Db	139295	CAGAATTCATATCCAGCCAAACCAAGCTTCCTAAGTGAAGGAGAAATAAATTCCTCTAC	139354	Db	140375	GATGTTCTTTGAAACCAATGAGAACAAAGACACAATGTACCAGAATCTCTGGGGCATATT	140434
QY	3241	AGAGAAGCAATGCTCAGAGATTTTGTACACACAGGCTGCTTACAGAGCTCCTGA	3300	QY	4321	TAAAGCAGTCTAGAGGAAATTTATAGCACTAGATGCTTACAGAGAAAGCAGCAAT	4380
Db	139355	AGAGAAGCAATGCTCAGAGATTTTGTACACACAGGCTGCTTACAGAGCTCCTGA	139414	Db	140435	TAAAGCAGTCTAGAGGAAATTTATAGCACTAGATGCTTACAGAGAAAGCAGCAAT	140494
QY	3301	AGGAAGCACAACATGAAAGGAACAACCTGGTACCAGCCACTGCAAAAAACATCCCAAAAT	3360	QY	4381	ATCTAAATAGACACCTTAACTCAATTTAAAGAACTTAGAGAGAAAGAGCAACAAA	4440
Db	139415	AGGAAGCACAACATGAAAGGAACAACCTGGTACCAGCCACTGCAAAAAACATCCCAAAAT	139474	Db	140495	ATCTAAATAGACACCTTAACTCAATTTAAAGAACTTAGAGAGAAAGAGCAACAAA	140554
QY	3361	GTAAGAGCAATGATGCTATGAAGAAAGTGCATCAACTAACGGGCAAAAATAACAGCTAG	3420	QY	4441	TTCAAAGCTAGCAGAGAACAGAAATAACTAAGATCAGAGCAGAACTGAAGAGATAGA	4500
Db	139475	GTAAGAGCAATGATGCTATGAAGAAAGTGCATCAACTAACGGGCAAAAATAACAGCTAG	139534	Db	140555	TTCAAAGCTAGCAGAGAACAGAAATAACTAAGATCAGAGCAGAACTGAAGAGATAGA	140614
QY	3421	TGTCATAATGGCAGGATCAAAATTCACACATATAATTAATTAATTTAAATGGGCT	3480	QY	4501	GACACAAAAGCCCTTCAATTAATCAATGAATCCAGGAGCTGGTTTTTGTGAAAGATCA	4560
Db	139535	TGTCATAATGGCAGGATCAAAATTCACACATATAATTAATTTAAATGGGCT	139594	Db	140615	GACACAAAAGCCCTTCAATTAATCAATGAATCCAGGAGCTGGTTTTTGTGAAAGATCA	140674
QY	3481	AAATTCCTCAATTAAGAGACAGACTGGCAAAATGGATAAAGAGTCAAGACCCATCAGT	3540	QY	4561	GCAAAATACACCACTAGACAGACTAATAAAGAAAGAAAGAGAGAAATCAAGAGATGC	4620
Db	139595	AAATTCCTCAATTAAGAGACAGACTGGCAAAATGGATAAAGAGTCAAGACCCATCAGT	139654	Db	140675	GCAAAATACACCACTAGACAGACTAATAAAGAAAGAAAGAGAGAAATCAAGAGATGC	140734
QY	3541	GTGCTGTATTCAGGAGGCCCATCTCACATGAAAAGACACACATAGGCTCAAAATAAAGGG	3600	QY	4621	ATAAATAATGATAAGGGGATATCACACCAGTCCACAGAAATACAAACTATTATCAG	4680
Db	139655	GTGCTGTATTCAGGAGGCCCATCTCACATGAAAAGACACACATAGGCTCAAAATAAAGGG	139714	Db	140735	ATAAATAATGATAAAGGGGATATCACACCAGTCCACAGAAATACAAACTATTATCAG	140794
QY	3601	ATGGAGGAGATTTACCAAGTAAATGGGAAACAAAAAAGCAGGGGTGCAATCCT	3660	QY	4681	AGAATATTATAACACCTCTATGCAATTAATAGAAAATCTAGAGAAATGGATAAAT	4740
Db	139715	ATGGAGGAGATTTACCAAGTAAATGGGAAACAAAAAAGCAGGGGTGCAATCCT	139774	Db	140795	AGAATATTATAACACCTCTATGCAATTAATAGAAAATCTAGAGAAATGGATAAAT	140854
QY	3661	AGTCTCTGATAAAGAGCTTTAAACCAACAAGATCAAAAGAGACAAAGAGGCCATTA	3720	QY	4741	CCTGACACATATGAGCCTGTATGACCTTGGGGACAGAAACAAAAGGGGTGAATGCA	4800
Db	139775	AGTCTCTGATAAAGAGCTTTAAACCAACAAGATCAAAAGAGACAAAGAGGCCATTA	139834	Db	140855	CCTGACACATATGAGCCTGTATGACCTTGGGGACAGAAACAAAAGGGGTGAATGCA	140914
QY	3721	CATAATGTPAAGGCATCAATGGAACAAGAGAGCTTAATCTCTAAATATACATGCACC	3780	QY	4801	GAATAAAGACAAAGACAAAAAGATATGTTTGAAGTAGGGGTACAGGGGCAACTTGCC	4860
Db	139835	CATAATGTPAAGGCATCAATGGAACAAGAGAGCTTAATCTCTAAATATACATGCACC	139894	Db	140915	GAATAAAGACAAAGACAAAAAGATATGTTTGAAGTAGGGGTACAGGGGCAACTTGCC	140974
QY	3781	CAATACAGAGCACCAGATTCATTAAGCAAGTCTTAGAGACCTACAAGAGACTTTGA	3840	QY	4861	TCATATGACAGAGGCCCTGAGCTTTACACCACCTCTCTATTATTATAGGCAAAAGAGAT	4920
Db	139895	CAATACAGAGCACCAGATTCATTAAGCAAGTCTTAGAGACCTACAAGAGACTTTGA	139954	Db	140975	TCATATGACAGAGGCCCTGAGCTTTACACCACCTCTCTATTATTATAGGCAAAAGAGAT	141034
QY	3841	CTCCACACAATAATAGTGGAGTCTAAATAATAATAGACACTTTAAACACCCCACTGCC	3900	QY	4921	ACCGAGAGGTCAGTTGGAAGAAGAGGTGAGCTGTTAGTCCAGAGTAGGCTGCAAGAC	4980
Db	139955	CTCCACACAATAATAGTGGAGTCTAAATAATAATAGACACTTTAAACACCCCACTGCC	140014	Db	141035	ACCGAGAGGTCAGTTGGAAGAAGAGGTGAGCTGTTAGTCCAGAGTAGGCTGCAAGAC	141094
QY	3901	AATATPAGCAGATCAATGAGACAGAAAAATTAACAAGGATATCCAGGAGTTGAAGTAC	3960	QY	4981	TGCATTCCTCAACAAATAGGCTCTAGATGCCAGTAGATAACCTCAAGAGGCCAGTGCC	5040
Db	140015	AATATPAGCAGATCAATGAGACAGAAAAATTAACAAGGATATCCAGGAGTTGAAGTAC	140074	Db	141095	TGCATTCCTCAACAAATAGGCTCTAGATGCCAGTAGATAACCTCAAGAGGCCAGTGCC	141154
QY	3961	TCGAGCAGGAGGACCTAATAGATATCTACAGAACTCCCAACCCCAATCAACAGATA	4020	QY	5041	AGGGAGTATGATGCCCTCAGCAAACTCTAGGGCAGGACAGAACTGAGCTTTGCCACAT	5100
Db	140075	TCGAGCAGGAGGACCTAATAGATATCTACAGAACTCCCAACCCCAATCAACAGATA	140134	Db	141155	AGGGAGTATGATGCCCTCAGCAAACTCTAGGGCAGGACAGAACTGAGCTTTGCCACAT	141214
QY	4021	TACACTCTTCTCAGCATCACATTTACACCTATTATTAATTTGAAGTAAATTTAAGTAA	4080	QY	5101	TCGTATTACCATTAACAGATTTGCTGTTTGTATCAAGTAGCTCCAGTGGAAATGCTGAGT	5160
Db	140135	TACACTCTTCTCAGCATCACATTTACACCTATTATTAATTTGAAGTAAATTTAAGTAA	140194	Db	141215	TCGTATTACCATTAACAGATTTGCTGTTTGTATCAAGTAGCTCCAGTGGAAATGCTGAGT	141274
QY	4081	ACACTCTCTCAGCAATGCAAAAGACAGAAATCTTAACAAACAGTCTCTCAGATACAG	4140	QY	5161	TGGTCATGATCCTTTGGCCTTTTGGCTCCCAAAACACATACACCTCTCAAGACTAA	5220
Db	140195	ACACTCTCTCAGCAATGCAAAAGACAGAAATCTTAACAAACAGTCTCTCAGATACAG	140254	Db	141275	TGGTCATGATCCTTTGGCCTTTTGGCTCCCAAAACACATACACCTCTCAAGACTAA	141334
QY	4141	TGCAATCTATTAGAACTCAGAAATTAAGAACTCACTCAAAATCAACAACTACATGGAA	4200	QY	5221	CCAGAGAAAGTCAAAATCCCTGAATATACCACTAAACAGTTCTTAAATTTGAAGCAGTAAT	5280
Db	140255	TGCAATCTATTAGAACTCAGAAATTAAGAACTCACTCAAAATCAACAACTACATGGAA	140314	Db	141335	CCAGAGAAAGTCAAAATCCCTGAATATACCACTAAACAGTTCTTAAATTTGAAGCAGTAAT	141394
QY	4201	ACTGAACACCTGCTCCTGAATGACTACTGGGTAATTAACAAATTAAGAGCAAAATAAA	4260	QY	5281	TGATAGCCTTACCAACCAAAAAAAGTCCAGGACAGACGATTCACAGCCAAATTTTACCA	5340
Db	140315	ACTGAACACCTGCTCCTGAATGACTACTGGGTAATTAACAAATTAAGAGCAAAATAAA	140374	Db	141395	TGATAGCCTTACCAACCAAAAAAAGTCCAGGACAGACGATTCACAGCCAAATTTTACCA	141454
				QY	5341	GAGGTACAAAGAGAGAGCTGGTACTATTCTCTGAACTATTCTCCAAAAATAGAAAATGG	5400



[illegible]

Db	142535	AATTTTCATATGGAACCAAAAAAGAGAGCCCAAGAGCCCAAGACAAATCTTAAAGCAAAAGAA	142595
Qy	6481	CAAAAGCTGGAGGTATCATGCTACCTGACTTAAACTATACTATAAGGCTACAGTAAACAA	6540
Db	142595	CAAAAGCTGGAGGTATCATGCTACCTGACTTAAACTATACTATAAGGCTACAGTAAACAA	142654
Qy	6541	AACTGCGATGGTACTGGGTACCAAAACAGATATATAGACCAATGGACAGAACAGACCTTC	6600
Db	142655	AACTGCGATGGTACTGGGTACCAAAACAGATATATAGACCAATGGACAGAACAGACCTTC	142714
Qy	6601	AGAAATTACACTGCAACTCTACATCCATCTGATCTTTTGACAAACCTTGACAAAAACAGCAA	6660
Db	142715	AGAAATTACACTGCAACTCTACATCCATCTGATCTTTTGACAAACCTTGACAAAAACAGCAA	142774
Qy	6661	TGGA AAAAGGATTCCTTATTTAAATAAATGGTGTGGAAAAACTGGCTAGCCATATGCAGA	6720
Db	142775	TGGA AAAAGGATTCCTTATTTAAATAAATGGTGTGGAAAAACTGGCTAGCCATATGCAGA	142834
Qy	6721	AAGCTGAAACTGGATGCCCTTCCTTTACACTCTTATACAAAGTTTAACATCAAGATGAATAAA	6780
Db	142835	AAGCTGAAACTGGATGCCCTTCCTTTACACTCTTATACAAAGTTTAACATCAAGATGAATAAA	142894
Qy	6781	GACTTAAATATAAGACATAAAACCATATAAAACCCAGAGAAAACTTAGGCAATACCATTC	6840
Db	142895	GACTTAAATATAAGACATAAAACCATATAAAACCCAGAGAAAACTTAGGCAATACCATTC	142954
Qy	6841	AGGATATGGACATGGGCAAGACTTCATGACTTAAACACACAAAAGCAATGGCAACAAAAG	6900
Db	142955	AGGATATGGACATGGGCAAGACTTCATGACTTAAACACACAAAAGCAATGGCAACAAAAG	143014
Qy	6901	CCAAAAATAGCAAGTGGGATCTGATTTAAACTATAGAGCTTCTGCACAGCAAAAAAAACT	6960
Db	143015	CCAAAAATAGCAAGTGGGATCTGATTTAAACTATAGAGCTTCTGCACAGCAAAAAAAACT	143074
Qy	6961	GTCTACAGAGTGAACAGCAACCTACAGATGGGAGAAAAATTTTTCGAATCTATCGATCT	7020
Db	143075	GTCTACAGAGTGAACAGCAACCTACAGATGGGAGAAAAATTTTTCGAATCTATCGATCT	143134
Qy	7021	GACAAAGGCTAATATCCAGAGATCTACAGAAACTTTAAACAAATTTTACAGAAAAAAACA	7080
Db	143135	GACAAAGGCTAATATCCAGAGATCTACAGAAACTTTAAACAAATTTTACAGAAAAAAACA	143194
Qy	7081	ACCCCGTCAAAATATGGGCAAGGATATAGCAGACACTTCTCAAAGAGACATTTATG	7140
Db	143195	ACCCCGTCAAAATATGGGCAAGGATATAGCAGACACTTCTCAAAGAGACATTTATG	143254
Qy	7141	CAGCCAACAAACATATGAAAAACCTCATCATCATTTGGTCCTTAGAGAAATGCAAAACA	7200
Db	143255	CAGCCAACAAACATATGAAAAACCTCATCATCATTTGGTCCTTAGAGAAATGCAAAACA	143314
Qy	7201	AAACCACAGTGACATACCATCTCATGCTAGTTAGAAATGGTGATCACTAAAAAGTCAGGAA	7260
Db	143315	AAACCACAGTGACATACCATCTCATGCTAGTTAGAAATGGTGATCACTAAAAAGTCAGGAA	143374
Qy	7261	ACAACAAATGCTGGAGAGGATGTGGAGAAATAGGAACACTTTTCCACTGTTGGTGGGAAT	7320
Db	143375	ACAACAAATGCTGGAGAGGATGTGGAGAAATAGGAACACTTTTCCACTGTTGGTGGGAAT	143434
Qy	7321	GTAATTTAGTTTCAACCAATGTGGAAAGACAGTGTGGAGATTCCTTAAAGGATATGAATCAT	7380
Db	143435	GTAATTTAGTTTCAACCAATGTGGAAAGACAGTGTGGAGATTCCTTAAAGGATATGAATCAT	143494
Qy	7381	AAATATCATTTTGACCCGCAATCCCATTTACTCAGTATATACCCAAAGGAATATAAATCAT	7440
Db	143495	AAATATCATTTTGACCCGCAATCCCATTTACTCAGTATATACCCAAAGGAATATAAATCAT	143554
Qy	7441	TCTATTATAAGACACATGCACATATGTTTATTGTCAGCACTGTATCACAATAGCAAGA	7500
Db	143555	TCTATTATAAGACACATGCACATATGTTTATTGTCAGCACTGTATCACAATAGCAAGA	143614
Qy	7501	CTTGGAAACCAACCCAAATGTCCATCAGTGATAGCTGGATAAGAAAAACATGGCCACATAT	7560
Db	143615	CTTGGAAACCAACCCAAATGTCCATCAGTGATAGCTGGATAAGAAAAACATGGCCACATAT	143674

QY	7561	ACACCATGAATACTATGACGCATATAAAGAGTGGTTTCATGCTCCTTTGCGAGAGATATG	7620	QY	8641	CAAGGTGTGTCTGGCTCCCATGTGAACCGCAGGAGACCTGTGATCTTTGCTTGAA	8700
Db	143675	ACACCATGAATACTATGACGCATATAAAGAGTGGTTTCATGCTCCTTTGCGAGAGATATG	143734	Db	144755	CAAGGTGTGTCTGGCTCCCATGTGAACCGCAGGAGACCTGTGATCTTTGCTTGAA	144814
QY	7621	GATGAAGCTGGAAACCATCATTTCTCAGCAAACTAACACAAGAACAGAAACCAACACCA	7680	QY	8701	CTTTTGTCTCAGTGAAGTTAGATGCCTGGAGTCCCTCGCACTCATGATCAGGTCCTG	8760
Db	143735	GATGAAGCTGGAAACCATCATTTCTCAGCAAACTAACACAAGAACAGAAACCAACACCA	143794	Db	144815	CTTTTGTCTCAGTGAAGTTAGATGCCTGGAGTCCCTCGCACTCATGATCAGGTCCTG	144874
QY	7681	CATGTTCTCAGTGAAGTGGAGTTGAACAATGAGAACACATGGACAGAGGGGAA	7740	QY	8761	CACATTCCTTTTCATTTAGAAATTTGCCATGCTGTTCCATAGACGGTCCAGTCCAGCAGG	8820
Db	143795	CATGTTCTCAGTGAAGTGGAGTTGAACAATGAGAACACATGGACAGAGGGGAA	143854	Db	144875	CACATTCCTTTTCATTTAGAAATTTGCCATGCTGTTCCATAGACGGTCCAGTCCAGCAGG	144934
QY	7741	CATCACACACAGGTCCTGTTGTGGTGGGACTAGGGAAGGATAGCATTTAGGAGAA	7800	QY	8821	AATAAATCACTGATTTGTTTAAATGTTCAATCAAGTTAGGCACTCTGCTGATCAGAAAT	8880
Db	143855	CATCACACACAGGTCCTGTTGTGGTGGGACTAGGGAAGGATAGCATTTAGGAGAA	143914	Db	144935	AATAAATCACTGATTTGTTTAAATGTTCAATCAAGTTAGGCACTCTGCTGATCAGAAAT	144994
QY	7801	ATACCTAAATGTAGATGACGGTGTGATGGTGAGCAAGCCACCATGGCACATGTATACCT	7860	QY	8881	GGAAGATGAGATCTGTTTGTAGAAAACTTCAAAGACTTCTCAGTACAAAGTTGGCGAG	8940
Db	143915	ATACCTAAATGTAGATGACGGTGTGATGGTGAGCAAGCCACCATGGCACATGTATACCT	143974	Db	144995	GGAAGATGAGATCTGTTTGTAGAAAACTTCAAAGACTTCTCAGTACAAAGTTGGCGAG	145054
QY	7861	ATGTAAACACCTGCACATCTGCACATGTACCCACACACTTAAAGTATTAATAAAAAA	7920	QY	8941	GGGTGGAGGAGGAATACCCCTAAGAAAGTCTTTAGGGAGACAAAGTGTCAAGAAATTTT	9000
Db	143975	ATGTAAACACCTGCACATCTGCACATGTACCCACACACTTAAAGTATTAATAAAAAA	144034	Db	145055	GGGTGGAGGAGGAATACCCCTAAGAAAGTCTTTAGGGAGACAAAGTGTCAAGAAATTTT	145114
QY	7921	CACACAACATGTTGCCCTGATGAAGGTCATTTAGTGCCCATAAATAAGTAAAAATGTTTT	7980	QY	9001	GATATTGTTAAAGCTAGTCCAAAGCCAGTTTGTATGTTGATTTCTATTATCATCTCCTG	9060
Db	144035	CACACAACATGTTGCCCTGATGAAGGTCATTTAGTGCCCATAAATAAGTAAAAATGTTTT	144094	Db	145115	GATATTGTTAAAGCTAGTCCAAAGCCAGTTTGTATGTTGATTTCTATTATCATCTCCTG	145174
QY	7981	ATGTTTTTATATTTGTTAAACATATAATATCCTTTACCATTAAACAAATCAGGTGCC	8040	QY	9061	CAATTCATTTGACATTAACATAGGTACCTTGGAAAGGGTTGGGGTTTGACTCCCATAGC	9120
Db	144095	ATGTTTTTATATTTGTTAAACATATAATATCCTTTACCATTAAACAAATCAGGTGCC	144154	Db	145175	CAATTCATTTGACATTAACATAGGTACCTTGGAAAGGGTTGGGGTTTGACTCCCATAGC	145234
QY	8041	ACTAAATCTTGTATATTAATACCTGTGTATCAATACAGCATTTCTTAATCAATAAGT	8100	QY	9121	TTTGGCAAGAATTTCTCAAGATGAATTAATGCTATTTCCTCAAGACTATCTGGCTGTA	9180
Db	144155	ACTAAATCTTGTATATTAATACCTGTGTATCAATACAGCATTTCTTAATCAATAAGT	144214	Db	145235	TTTGGCAAGAATTTCTCAAGATGAATTAATGCTATTTCCTCAAGACTATCTGGCTGTA	145294
QY	8101	ATATCATTAATTTTAAATTCATAAGTTTAAACATAATTTCTTAATTAGTAGTAAATA	8160	QY	9181	AAAGAGATTTGAGAACTAGGGGATCAGGAGAGGAAATTAATTTCTAAAGAACTGAGCAT	9240
Db	144215	ATATCATTAATTTTAAATTCATAAGTTTAAACATAATTTCTTAATTAGTAGTAAATA	144274	Db	145295	AAAGAGATTTGAGAACTAGGGGATCAGGAGAGGAAATTAATTTCTAAAGAACTGAGCAT	145354
QY	8161	GAAAGCAACCTTCTCCCTGCAGTGGCCTTCATTTAGTGAATATTAGCATTTACATAG	8220	QY	9241	ATGATTAATATTCCTTTGTTTAAAGAACTGTTTATCAAGCCCTAATTAATTTCTGATGACT	9300
Db	144275	GAAAGCAACCTTCTCCCTGCAGTGGCCTTCATTTAGTGAATATTAGCATTTACATAG	144334	Db	145355	ATGATTAATATTCCTTTGTTTAAAGAACTGTTTATCAAGCCCTAATTAATTTCTGATGACT	145414
QY	8221	ACATATACCTTGTAATTTCCATCTCTGTTTCTTAATATACATAGTACAGATTAATATT	8280	QY	9301	GGCAGCTGTAAATCAGAGCTTTGTCGATTTTCTCATTTGACGGCAACAAAGAGTG	9360
Db	144335	ACATATACCTTGTAATTTCCATCTCTGTTTCTTAATATACATAGTACAGATTAATATT	144394	Db	145415	GGCAGCTGTAAATCAGAGCTTTGTCGATTTTCTCATTTGACGGCAACAAAGAGTG	145474
QY	8281	ATTTACTTTTATGTTTATGATCCCGTTAGCCCTTTATTTTGGATTTTGTCCCATTTTCT	8340	QY	9361	TGTGCTTTGGGATAAGCAAGAGCCTGGGCAAGTTTCTAACTGGTCTCTGATGTTTC	9420
Db	144395	ATTTACTTTTATGTTTATGATCCCGTTAGCCCTTTATTTTGGATTTTGTCCCATTTTCT	144454	Db	145475	TGTGCTTTGGGATAAGCAAGAGCCTGGGCAAGTTTCTAACTGGTCTCTGATGTTTC	145534
QY	8341	TTTAGATTTAACTTGGTCATGGCACCAATTAACAATCTATAGCATTTTACAGTTT	8400	QY	9421	AGGGATTTTCTGTTGTTTATATTAAGCAAGCTGAGCACCGTATATATGTTTGTCTG	9480
Db	144455	TTTAGATTTAACTTGGTCATGGCACCAATTAACAATCTATAGCATTTTACAGTTT	144514	Db	145535	AGGGATTTTCTGTTGTTTATATTAAGCAAGCTGAGCACCGTATATATGTTTGTCTG	145594
QY	8401	GAATAATTTGCACAGCAGCTATTTTCTTTTCTTTTACCTCTCAGACAAATCTTTCACA	8460	QY	9481	ATAACAAGAGAAAAATGAATTTGGCAGACACCTTTTCCACAGACACAGGAGAGCAGCTAT	9540
Db	144515	GAATAATTTGCACAGCAGCTATTTTCTTTTCTTTTACCTCTCAGACAAATCTTTCACA	144574	Db	145595	ATAACAAGAGAAAAATGAATTTGGCAGACACCTTTTCCACAGACACAGGAGAGCAGCTAT	145654
QY	8461	TGGTGAAAGGTATCATTTATCCCACTTTTACTGAGATTTCTAAAGGAGGATAAGTACC	8520	QY	9541	TTGAACAAAGTGGAAATTTGGACTGCTTACTGGATGATCAGACACTGATGTTCAAGCT	9600
Db	144575	TGGTGAAAGGTATCATTTATCCCACTTTTACTGAGATTTCTAAAGGAGGATAAGTACC	144634	Db	145655	TTGAACAAAGTGGAAATTTGGACTGCTTACTGGATGATCAGACACTGATGTTCAAGCT	145714
QY	8521	TTGTCCAGGGTCTCCCTGACTTGGACCTGGGACACAGACCTGGGATCAGACATTTAA	8580	QY	9601	TTCAATCATGTAATAGTCTTAGGTTTCAAGTACACAGCATTTCAAGAGAGGAAGCA	9660
Db	144635	TTGTCCAGGGTCTCCCTGACTTGGACCTGGGACACAGACCTGGGATCAGACATTTAA	144694	Db	145715	TTCAATCATGTAATAGTCTTAGGTTTCAAGTACACAGCATTTCAAGAGAGGAAGCA	145774
QY	8581	GCTCTAGCATATCTGACTTCCAGGCTCTCTAACATGCTTCAATTTCTTTTATGCT	8640	QY	9661	GGCTGATTTGAGGGCATGTAGAAAAATGAAAAGCCTTTATCTGAGAAAACCAACTGGGG	9720
Db	144695	GCTCTAGCATATCTGACTTCCAGGCTCTCTAACATGCTTCAATTTCTTTTATGCT	144754	Db	145775	GGCTGATTTGAGGGCATGTAGAAAAATGAAAAGCCTTTATCTGAGAAAACCAACTGGGG	145834
				QY	9721	TTATAGGTTATCTGCTGCTACCTTTTAAAGGAGGAACACTGAAATTAATATAGGACTGAA	9780

Db	145835	TTATAGGTTATCTGGTCACCTTTAAAGGGAAGAACACTGAATTAATATAGGAGCTGAA	145894	Db	146915	AGCAAAATATCTTGGAGAGGGATAACATATATTTCTCCCTGAGTAATTAATCTCAACCT	146974
Qy	9781	GGCAGCTGTTAATAGTACCCCTCACACACACTTTCTTATTTCTGAGCTAGATTAC	9840	Qy	10861	GCAGGCAATATCACAGCAGCTGGCTGGCATTTGTAACAGAAGGACTGATATCAAGTCCCAA	10920
Db	145895	GGCAGCTGTTAATAGTACCCCTCACACACACTTTCTTATTTCTGAGCTAGATTAC	145954	Db	146975	GCAGGCAATATCACAGCAGCTGGCTGGCATTTGTAACAGAAGGACTGATATCAAGTCCCAA	147034
Qy	9841	AGCTGGAAGCACAAACCAAGAAATAACAAATCCACTGGGGGCAACACAGCATTTCTTAAC	9900	Qy	10921	GACACAGTACTCAGTTTAAAGACATATAATGACAAACAGCTCAACAGTGTATATTAAGA	10980
Db	145955	AGCTGGAAGCACAAACCAAGAAATAACAAATCCACTGGGGGCAACACAGCATTTCTTAAC	146014	Db	147035	GACACAGTACTCAGTTTAAAGACATATAATGACAAACAGCTCAACAGTGTATATTAAGA	147094
Qy	9901	ACCTATGGGTGCAAAATGGGATCTTGACTCTCTCCACTCTGAAACACACAAAGCCA	9960	Qy	10981	AGTTAAGCTTGAAGGTGACAAAAGCTGGGTTAGTGGGAGTTTATAACATGCTCATGA	11040
Db	146015	ACCTATGGGTGCAAAATGGGATCTTGACTCTCTCCACTCTGAAACACACAAAGCCA	146074	Db	147095	AGTTAAGCTTGAAGGTGACAAAAGCTGGGTTAGTGGGAGTTTATAACATGCTCATGA	147154
Qy	9961	GGGAAACTTGACGCTCTACTAAATGGAGTGTGACTGAGCCAAATGGTGGGTTTCATACCAC	10020	Qy	11041	ATTTTGAATAATGCAATCATGATATCTGTCATATTTACTTCAAAATAGATCGTCTGTGA	11100
Db	146075	GGGAAACTTGACGCTCTACTAAATGGAGTGTGACTGAGCCAAATGGTGGGTTTCATACCAC	146134	Db	147155	ATTTTGAATAATGCAATCATGATATCTGTCATATTTACTTCAAAATAGATCGTCTGTGA	147214
Qy	10021	CATACAAATCAAGATGCTCAGTTTGGCAATTTACCTCATCAACAAAGATATTTAACTA	10080	Qy	11101	GACTCTAGGGTTACTATGAGGTGTACTGAGTGTGACGTTTGAAGTTTACAGAACTAAATAG	11160
Db	146135	CATACAAATCAAGATGCTCAGTTTGGCAATTTACCTCATCAACAAAGATATTTAACTA	146194	Db	147215	GACTCTAGGGTTACTATGAGGTGTACTGAGTGTGACGTTTGAAGTTTACAGAACTAAATAG	147274
Qy	10081	CAGTACTCAGCTTGTGCCAATAAAGCTCTGAATAATCTTCACCATAAAGCTATTAC	10140	Qy	11161	TTAAATCATTTTGACAGCACCTTAGAGGATTTAGAGGATTTAGTACATGTTTCAAGCTTGC	11220
Db	146195	CAGTACTCAGCTTGTGCCAATAAAGCTCTGAATAATCTTCACCATAAAGCTATTAC	146254	Db	147275	TTAAATCATTTTGACAGCACCTTAGAGGATTTAGTACATGTTTCAAGCTTGCATGTC	147334
Qy	10141	ACTAATAAACAATACAGGACGAAAGCTATCTGCTGAGCTGCTGCTTCTTGTATTAGAG	10200	Qy	11221	AGAAACATATGGAAGCCCTGGGTGGGCACACTACATTTTCAGAGCATGGCATTTAGCATGG	11280
Db	146255	ACTAATAAACAATACAGGACGAAAGCTATCTGCTGAGCTGCTGCTTCTTGTATTAGAG	146314	Db	147335	AGAAACATATGGAAGCCCTGGGTGGGCACACTACATTTTCAGAGCATGGCATTTAGCATGG	147394
Qy	10201	AATATAAATAAAGGCTTTAAGGCTTTGAAGCTTTCTCAAAATTAATGAGTACCTAGGAA	10260	Qy	11281	GTATCATCATGACACAGATGGGCCCTTGTCTGCTTGGGAGTACCTTGGCCCATGTCGCA	11340
Db	146315	AATATAAATAAAGGCTTTAAGGCTTTGAAGCTTTCTCAAAATTAATGAGTACCTAGGAA	146374	Db	147395	GTATCATCATGACACAGATGGGCCCTTGTCTGCTTGGGAGTACCTTGGCCCATGTCGCA	147454
Qy	10261	CACAAGTACGTTTTCAGGACAAATGCATTAATATAACCCAAATCATTAAGATTTAAGA	10320	Qy	11341	AGTTTGGCCCTTTGGCAGGAGGCCCTGATCTGAAGCTAGATTTGAGAGGAGAGAGTCTG	11400
Db	146375	CACAAGTACGTTTTCAGGACAAATGCATTAATATAACCCAAATCATTAAGATTTAAGA	146434	Db	147455	AGTTTGGCCCTTTGGCAGGAGGCCCTGATCTGAAGCTAGATTTGAGAGGAGAGAGTCTG	147514
Qy	10321	TTCTTCTCTTTTTTTTTTTTTTTTTTTTTTTTGGAGATGAGTTTCAGTCTCTTCCGCCAGGC	10380	Qy	11401	CAGTTTCTAATACCTTAAACAAGAGGTTCACTTAAGTGTAGTGTAGTGTAGTGTAGTGTAG	11460
Db	146435	TTCTTCTCTTTTTTTTTTTTTTTTTTTTTTTTGGAGATGAGTTTCAGTCTCTTCCGCCAGGC	146494	Db	147515	CAGTTTCTAATACCTTAAACAAGAGGTTCACTTAAGTGTAGTGTAGTGTAGTGTAGTGTAG	147574
Qy	10381	TAGATGCAATGTTGATCCCGGTCACCTGCAACCTCCACCTCCCGGGTTCAAGTGAAT	10440	Qy	11461	TGTAATCAGAACTGAGAAAGCCAGACGAGCTCTCATCTAATTTCCACCCACATCTGCTTT	11520
Db	146495	TAGATGCAATGTTGATCCCGGTCACCTGCAACCTCCACCTCCCGGGTTCAAGTGAAT	146554	Db	147575	TGTAATCAGAACTGAGAAAGCCAGACGAGCTCTCATCTAATTTCCACCCACATCTGCTTT	147634
Qy	10441	CTCCTGCCCTCAGCTCCCAAGTAGCTGGGACTACAGGCACGTCGCCACCGCTGGCTAA	10500	Qy	11521	GTACTTTATAGTCTTCAGATGCTTCAATCCACGAGTATCCCGAGTGTGAAGAGCACA	11580
Db	146555	CTCCTGCCCTCAGCTCCCAAGTAGCTGGGACTACAGGCACGTCGCCACCGCTGGCTAA	146614	Db	147635	GTACTTTATAGTCTTCAGATGCTTCAATCCACGAGTATCCCGAGTGTGAAGAGCACA	147694
Qy	10501	TTTTTGTATTTTAGTAGAGATGGTTTCCCGACGTTGGCCAGGCTGGTCTTGAACCTCT	10560	Qy	11581	TGTGTATCATTTGCCATTTGCAAGATGAGTGAATTAACCTTTTATAGCAGCTATATAA	11640
Db	146615	TTTTTGTATTTTAGTAGAGATGGTTTCCCGACGTTGGCCAGGCTGGTCTTGAACCTCT	146674	Db	147695	TGTGTATCATTTGCCATTTGCAAGATGAGTGAATTAACCTTTTATAGCAGCTATATAA	147754
Qy	10561	GACCTCAGGTGATCTGCCCTCCCTCAGCTCCCAAAATGCTGGGATTTACAGGCATGAGCCA	10620	Qy	11641	CATTTACTGTTCTGGATCATCTTTATTTCTTTTGCATTTTACCTAGCATTTTCAACACC	11700
Db	146675	GACCTCAGGTGATCTGCCCTCCCTCAGCTCCCAAAATGCTGGGATTTACAGGCATGAGCCA	146734	Db	147755	CATTTACTGTTCTGGATCATCTTTATTTCTTTTGCATTTTACCTAGCATTTTCAACACC	147814
Qy	10621	CTGGGCCGCTCTCTCCTTAACCTTAACACAGGCTGTTTTCAGCACACACAGTTTCTCA	10680	Qy	11701	AAATTTGTTTTTATTCCTTACAAATTTTCAATAGATTTTGGGGCAGGATTAAGTGTAA	11760
Db	146735	CTGGGCCGCTCTCTCCTTAACCTTAACACAGGCTGTTTTCAGCACACACAGTTTCTCA	146794	Db	147815	AAATTTGTTTTTATTCCTTACAAATTTTCAATAGATTTTGGGGCAGGATTAAGTGTAA	147874
Qy	10681	AGGAAAAAAGGCTCTCTTTTGTATCTTTTGTATCTTTATAGCCTTTTATAAATATGT	10740	Qy	11761	AACAGATAATGAATATATGATGATTAATTTTCAAGTGTTCCTTGGGAACCTCAAAATTT	11820
Db	146795	AGGAAAAAAGGCTCTCTTTTGTATCTTTTGTATCTTTTATAGCCTTTTATAAATATGT	146854	Db	147875	AACAGATAATGAATATATGATGATTAATTTTCAAGTGTTCCTTGGGAACCTCAAAATTT	147934
Qy	10741	ACACAGAGTCAATATTTTAAAGGATGCTAGTGAATATTTCTGAAACCTAAGTGACTACA	10800	Qy	11821	TATGGGATTAAGTGAGGAAACCTGAGGCCCTGGGAAGTTTAAAGTGGCTGGCTCCTCAGT	11880
Db	146855	ACACAGAGTCAATATTTTAAAGGATGCTAGTGAATATTTCTGAAACCTAAGTGACTACA	146914	Db	147935	TATGGGATTAAGTGAGGAAACCTGAGGCCCTGGGAAGTTTAAAGTGGCTGGCTCCTCAGT	147994
Qy	10801	AGCAAAATATCTTGGAGAGGGATACATATATTTCTCTCCCTGAGTAATTAATCTCAACCT	10860	Qy	11881	TGCCCTTCCATGTGGGCAAAAGCTGGGAACCAACCCACATCTTTTCTAGTCTCTGCAAGTTT	11940
				Db	147995	TGCCCTTCCATGTGGCAAAAGCTGGGAACCAACCCACATCTTTTCTAGTCTCTGCAAGTTT	148054

QY	11941	TCTGCTCTATTGCCCCTCTCTTGGTAGGAAAAACATCACAGACCATGAGGCTTCACCTTAAAG	12000
Db	148055	TCTGCTCTATTGCCCTCTCTTGGTAGGAAAAACATCACAGACCATGAGGCTTCACCTTAAAG	148114
QY	12001	GTGGGAAAGGACAGAGGAGAGAGACATCCACAAGTTCTAGCTATGAGGTTTCCAAAAA	12060
Db	148115	GTGGGAAAGGACAGAGGAGAGAGACATCCACAAGTTCTAGCTATGAGGTTTCCAAAAA	148174
QY	12061	ATAACAGAAAAAGAGATTTCTTGACTCTTTATATAGTTAGGTATTAATCATCAGCCCAAA	12120
Db	148175	ATAACAGAAAAAGAGATTTCTTGACTCTTTATATAGTTAGGTATTAATCATCAGCCCAAA	148234
QY	12121	ACTCCCTCCCTATTGCTAGAGAGGAAAACTCCTTGCAGCAATTTATTTCTGTTCTTT	12180
Db	148235	ACTCCCTCCCTATTGCTAGAGAGGAAAACTCCTTGCAGCAATTTATTTCTGTTCTTT	148294
QY	12181	TGGTCTCAATTTGAAAAATTTAGGTACTTTTTTTTCAATTAACAGAGTTTCAACATGTAA	12240
Db	148295	TGGTCTCAATTTGAAAAATTTAGGTACTTTTTTTTCAATTAACAGAGTTTCAACATGTAA	148354
QY	12241	AAACAAGTACTATTCTTTTACCTCAAAATCTGAAGTCAACAGTGTATTACTCTAACCTC	12300
Db	148355	AAACAAGTACTATTCTTTTACCTCAAAATCTGAAGTCAACAGTGTATTACTCTAACCTC	148414
QY	12301	ATATTTTCATGTATAATACAGATGCTCGTTGACTTATGATGGGGCTATATCCTGATAAC	12360
Db	148415	ATATTTTCATGTATAATACAGATGCTCGTTGACTTATGATGGGGCTATATCCTGATAAC	148474
QY	12361	CCATTGGAGGTTAAAAATTTTAAAGTTGAAAAATGCAATTAACCCGCCATTAACCCAC	12420
Db	148475	CCATTGGAGGTTAAAAATTTTAAAGTTGAAAAATGCAATTAACCCGCCATTAACCCAC	148534
QY	12421	TGAAAAGTAAAAAATAAATACTAAATCTAACCATCAATCAGGATATATCTGTACCAAT	12480
Db	148535	TGAAAAGTAAAAAATAAATACTAAATCTAACCATCAATCAGGATATATCTGTACCAAT	148594
QY	12481	TTATTAATACATCTCCTAACTCTTAAACTGTGATAAAATGCAAAATGTTTAAATACAAAAT	12540
Db	148595	TTATTAATACATCTCCTAACTCTTAAACTGTGATAAAATGCAAAATGTTTAAATACAAAAT	148654
QY	12541	CTACCTTAGAACAGAGAGTCAATTTTTTTTTCATTTTGTCTAGATGCTCAAGTGATTC	12600
Db	148655	CTACCTTAGAACAGAGAGTCAATTTTTTTTTCATTTTGTCTAGATGCTCAAGTGATTC	148714
QY	12601	TAGATGCTATAAATGTCCAGAAATCAGAGATAGGTATAGGCTTGTGCCATTCACAAAGT	12660
Db	148715	TAGATGCTATAAATGTCCAGAAATCAGAGATAGGTATAGGCTTGTGCCATTCACAAAGT	148774
QY	12661	AGTCAGGCGCTTGTGTGGTAAATTTAAATTTCAATTTAGTTTAAACTTAAATTTAAAAA	12720
Db	148775	AGTCAGGCGCTTGTGTGGTAAATTTAAATTTCAATTTAGTTTAAACTTAAATTTAAAAA	148834
QY	12721	TTTAGTTTCTATTGCTTACACATTTCAAGTCCCAACAGCCACATGTTGCTAGTGA	12780
Db	148835	TTTAGTTTCTATTGCTTACACATTTCAAGTCCCAACAGCCACATGTTGCTAGTGA	148894
QY	12781	CTACCATATGGAACATTTGCAATATAGGTATTTCTCTATCCTACACAGGAGATCTATTAGA	12840
Db	148895	CTACCATATGGAACATTTGCAATATAGGTATTTCTCTATCCTACACAGGAGATCTATTAGA	148954
QY	12841	CAGTCAGGTGTTTAGTCAAGCATCTCTGAGAAAAATTTAGAGAGGAAGAACAGAGAAAT	12900
Db	148955	CAGTCAGGTGTTTAGTCAAGCATCTCTGAGAAAAATTTAGAGAGGAAGAACAGAGAAAT	149014
QY	12901	TAACTATCTATTCTTTGATGCTTCTCTATGTTTGGCTGTTGCTGCTGCTAAATGGATA	12960
Db	149015	TAACTATCTATTCTTTGATGCTTCTCTATGTTTGGCTGTTGCTGCTGCTAAATGGATA	149074
QY	12961	CAGCCAGGCGCAAAATCATGAAAAACAGTGTAGTAAATTTTAAATAGGTCTACTATCTT	13020
Db	149075	CAGCCAGGCGCAAAATCATGAAAAACAGTGTAGTAAATTTTAAATAGGTCTACTATCTT	149134
QY	13021	TTAGGAAATATCTCTTCTTCTTATATACATATCAAGAGAAAGAACTGAAATATAGT	13080
Db	149135	TTAGGAAATATCTCTTCTTCTTATATACATATCAAGAGAAAGAACTGAAATATAGT	149194
QY	13081	TTCTTCTTAATTTGCTTACACATACGTTTTTCTTGGAAATCCTCCTTTAACAAAAATCACTA	13140
Db	149195	TTCTTCTTAATTTGCTTACACATACGTTTTTCTTGGAAATCCTCCTTTAACAAAAATCACTA	149254
QY	13141	CCCAAAATATCTTTTATATTTCTATGATGGGTTTCCAGGACACATGTTCTCCCAATGTTTTA	13200
Db	149255	CCCAAAATATCTTTTATATTTCTATGATGGGTTTCCAGGACACATGTTCTCCCAATGTTTTA	149314
QY	13201	AGCTGAAGGAATTTGAGAAAAACAAGAAAGCAAGATCACTCTGACCTTCCCTCCAC	13260
Db	149315	AGCTGAAGGAATTTGAGAAAAACAAGAAAGCAAGATCACTCTGACCTTCCCTCCAC	149374
QY	13261	CTCCATCTGGAAGGAGTCAATAAAACCTAGGATTTTCTGACCTTCCCATGTAGCAAGTCA	13320
Db	149375	CTCCATCTGGAAGGAGTCAATAAAACCTAGGATTTTCTGACCTTCCCATGTAGCAAGTCA	149434
QY	13321	TAAAGACCTCATGCGAGAGGTGCCCTCTGTTATACCCAGAAGAAAGAAATTTCCCCCGG	13380
Db	149435	TAAAGACCTCATGCGAGAGGTGCCCTCTGTTATACCCAGAAGAAAGAAATTTCCCCCGG	149494
QY	13381	CTTTTGTGTTGAGATGTTGTTTACTCTCTGTCACCCAGGCTAGAGTGCAGTTGCGATGTC	13440
Db	149495	CTTTTGTGTTGAGATGTTGTTTACTCTCTGTCACCCAGGCTAGAGTGCAGTTGCGATGTC	149554
QY	13441	ATGTTCTGCTGCAACCTTGAACCTCTGGGCTCAAGCAATTTCTCTGCTGACCTTCCCA	13500
Db	149555	ATGTTCTGCTGCAACCTTGAACCTCTGGGCTCAAGCAATTTCTCTGCTGACCTTCCCA	149614
QY	13501	GTAGCTCAGACACAGACACATCTCCACATTTGCTTACTTAAAAATTAATTCCTTTTTTT	13560
Db	149615	GTAGCTCAGACACAGACACATCTCCACATTTGCTTACTTAAAAATTAATTCCTTTTTTT	149674
QY	13561	TATTAATTTATTTATTTTTTTTTTAGAGATGGGGGGTCTCGCTATGTTGACCCGGTTGAT	13620
Db	149675	TATTAATTTATTTATTTTTTTTTTAGAGATGGGGGGTCTCGCTATGTTGACCCGGTTGAT	149734
QY	13621	CTTGAACCTCATAGCCTCAAGGATCATCCACCTTGGCTCTCAAGTGCCTGAGATTACA	13680
Db	149735	CTTGAACCTCATAGCCTCAAGGATCATCCACCTTGGCTCTCAAGTGCCTGAGATTACA	149794
QY	13681	GSCATGAGCCACTGCTCTGCGCTAAGAAATCCTTATCTCCAAAGACAAAGGTAGAACAAA	13740
Db	149795	GSCATGAGCCACTGCTCTGCGCTAAGAAATCCTTATCTCCAAAGACAAAGGTAGAACAAA	149854
QY	13741	TAAGAATCTGAACAAACAGGCTTCTAAATTTTCCCAAGTTTATTTACCATTAGATCATAC	13800
Db	149855	TAAGAATCTGAACAAACAGGCTTCTAAATTTTCCCAAGTTTATTTACCATTAGATCATAC	149914
QY	13801	TCTGCCCTATCATATTTCTCCACACTATCCACACTTTTATCAAACTTACTGTAAAAAAT	13860
Db	149915	TCTGCCCTATCATATTTCTCCACACTATCCACACTTTTATCAAACTTACTGTAAAAAAT	149974
QY	13861	ATCAGGTTGAACCACTTTTTTGGGTTCTTCTTACCAGGCGCTCTGTGCACGTAACAT	13920
Db	149975	ATCAGGTTGAACCACTTTTTTGGGTTCTTCTTACCAGGCGCTCTGTGCACGTAACAT	150034
QY	13921	ATTTCAATTAATAGTACACTTTTTCTTTGTTTATTTCTGCTGTTTGTATAGTGGCCTCAGC	13980
Db	150035	ATTTCAATTAATAGTACACTTTTTCTTTGTTTATTTCTGCTGTTTGTATAGTGGCCTCAGC	150094
QY	13981	CATGAACCTAGGAAGGTTGAAGAAAGTATTTTTCTCTACTCTATATCTAGTATATTC	14040
Db	150095	CATGAACCTAGGAAGGTTGAAGAAAGTATTTTTCTCTACTCTATATCTAGTATATTC	150154
QY	14041	AAGAGCATAGAAATGATTGTTTAGAAGAGGAAAAATTTCTTCAACAGGCTACCTACAAAC	14100
Db	150155	AAGAGCATAGAAATGATTGTTTAGAAGAGGAAAAATTTCTTCAACAGGCTACCTACAAAC	150214
QY	14101	TTTTGAGACGAAGAAATTAATAAGACAGTCAATTTTTTACTGACAGTGAACCCGCTCAA	14160

[illegible]





Db	154595	 TAATCAACATGTTAGAGAAAATCATTTTTTGTGTGCTGAATATGTTGTCAC	154654
Qy	18541	TGGGTCCTAGATGGCAGTATASCATAGTGGTTAAAGTGCCTTTGGAGCCGACGTAAGATTAC	18600
Db	154655	TGGGTCCTAGATGGCAGTATASCATAGTGGTTAAAGTGCCTTTGGAGCCGACGTAAGATTAC	154714
Qy	18601	AACTGCGTTCAATCAACATCATGGCTATGTTTCCCTTTTAAAGTAAAGTAAATTAATGGCT	18660
Db	154715	AACTGCGTTCAATCAACATCATGGCTATGTTTCCCTTTTAAAGTAAAGTAAATTAATGGCT	154774
Qy	18661	CTGAACCTCTGCTTCCCTCATATCAACATGTAATCATTTGAAGAATTTGAATGAACGTGC	18720
Db	154775	CTGAACCTCTGCTTCCCTCATATCAACATGTAATCATTTGAAGAATTTGAATGAACGTGC	154834
Qy	18721	CTGCACTCAATGCCAGCTATCTTACTAATCTTGAATTCATCTGTAATCTCCCTCTCACA	18780
Db	154835	CTGCACTCAATGCCAGCTATCTTACTAATCTTGAATTCATCTGTAATCTCCCTCTCACA	154894
Qy	18781	TTCTTTTCCCTTTAAAGTCAAAATGGACAAAATTTAAAAATATACTACGCTCTTCTCCCTCT	18840
Db	154895	TTCTTTTCCCTTTAAAGTCAAAATGGACAAAATTTAAAAATATACTACGCTCTTCTCCCTCT	154954
Qy	18841	TATGTTTTCTCTTTGGACATATATAAATGATTAATCAAGGGATATGGTCAGTGGGACT	18900
Db	154955	TATGTTTTCTCTTTGGACATATATAAATGATTAATCAAGGGATATGGTCAGTGGGACT	155014
Qy	18901	TCATCAACTTAAAGCACACAAATTTTCAAGCTTAAGTCAATCAATATTTACTTTGAATTT	18960
Db	155015	TCATCAACTTAAAGCACACAAATTTTCAAGCTTAAGTCAATCAATATTTACTTTGAATTT	155074
Qy	18961	CAATTCGCATTTATGTTTACATAAATTAGATTTGATTTGCTGTTCTCCAAAGTCCATCCA	19020
Db	155075	CAATTCGCATTTATGTTTACATAAATTAGATTTGATTTGCTGTTCTCCAAAGTCCATCCA	155134
Qy	19021	ATTATCCATCCATTTGGGAGCCAAATCTCTTATTGTTGGTCATACATACATGATATCTTC	19080
Db	155135	ATTATCCATCCATTTGGGAGCCAAATCTCTTATTGTTGGTCATACATACATGATATCTTC	155194
Qy	19081	TCACAAGACACAGTTTGAAGCAAGTCCCTTTTGTCTGCACAGAACCCACACCTTTCCC	19140
Db	155195	TCACAAGACACAGTTTGAAGCAAGTCCCTTTTGTCTGCACAGAACCCACACCTTTCCC	155254
Qy	19141	AATGCACGCCCTTGTGTGCACAGGCCACACAGAGGAATCCCATGAATGTTAGGCAGT	19200
Db	155255	AATGCACGCCCTTGTGTGCACAGGCCACACAGAGGAATCCCATGAATGTTAGGCAGT	155314
Qy	19201	TATCACCATGTCATTCTAAACTCTAGCCCTGGTAAATGCTCTTAGGCTTTAAACTGAAACT	19260
Db	155315	TATCACCATGTCATTCTAAACTCTAGCCCTGGTAAATGCTCTTAGGCTTTAAACTGAAACT	155374
Qy	19261	GCTTAAGGAGAGGAGAAAAGCCCTTTGGGACGACAGGTTCAAAAGTCTAAGGACAGTG	19320
Db	155375	GCTTAAGGAGAGGAGAAAAGCCCTTTGGGACGACAGGTTCAAAAGTCTAAGGACAGTG	155434
Qy	19321	TCAGTAGAATGTCATCTAAGGAAAATTCAGGAACAAAGTGTGGACCATGAGTCCACTAACC	19380
Db	155435	TCAGTAGAATGTCATCTAAGGAAAATTCAGGAACAAAGTGTGGACCATGAGTCCACTAACC	155494
Qy	19381	GCATCCCTGTTGCTCTTTTATCTACAACTGTGCTTTGATPTCAAGGGCAGGGATTT	19440
Db	155495	GCATCCCTGTTGCTCTTTTATCTACAACTGTGCTTTGATPTCAAGGGCAGGGATTT	155554
Qy	19441	ATCCCCAATTTGCATACGCTGAGCCAGGATCTCTGGGAACATAAATTAATGCCAAATAA	19500
Db	155555	ATCCCCAATTTGCATACGCTGAGCCAGGATCTCTGGGAACATAAATTAATGCCAAATAA	155614
Qy	19501	TCACTGTGCATAAATTTATTCGCTTTTCTCTCTTTGTAAGACATGTCATAACTTTTA	19560
Db	155615	TCACTGTGCATAAATTTATTCGCTTTTCTCTCTTTGTAAGACATGTCATAACTTTTA	155674
Qy	19561	GCTATAATCAATCCAGATTTAAATGAAATGAATCTCTGTTGGGAAAGGAACCATTTTTAT	19620





Db	158975	AGTCAAAGGCATATTCACCTACATCTCCTATGACTCCTCTCTATGACTCAACCAC	159034	Db	160055	ATAATCTGTATGAAAAGTGCTAAACATTTCCCTTTAATGTTGACGACACAGGTTTATGA	160114
QY	22921	TTTTCTGCGCCCTCTATTATAGACATTTACTTCATAGACCTGTGTTCTCTCTTTGAGAT	22980	QY	24001	TGCTTTGGGGTGGGGTGGAGGTGAGGACATATAGGAATAATGTTATTTTCTCTTAA	24060
Db	159035	TTTTCTGCGCCCTCTATTATAGACATTTACTTCATAGACCTGTGTTCTCTTTGAGAT	159094	Db	160115	TGCTTTGGGGTGGGGTGGAGGTGAGGACATATAGGAATAATGTTATTTTCTCTTAA	160174
QY	22981	AGTCCAACTTACAAGTGTCAACATGAGTGTGTTTTTTTTTTTACTTTTATGATGCTGCTTC	23040	QY	24061	ACAACGAGGGCTCTCAGCCTTTCTCAAGTGTTCATAAGTTCACACGAGGTCTTCATCCTT	24120
Db	159095	AGTCCAACTTACAAGTGTCAACATGAGTGTGTTTTTTTTTTTACTTTTACTTTTCTGATG	159154	Db	160175	ACAACGAGGGCTCTCAGCCTTTCTCAAGTGTTCATAAGTTCACACGAGGTCTTCATCCTT	160234
QY	23041	AGTGTGATGTTAATGGTGAGACCCATAAACCATCTCTGTTTTCACCTTTCAGTAAG	23100	QY	24121	ATGAATATTACAACTCAGTGTGATTTTCAGAAATCCCTCTCTATATAATCAGCACATAAT	24180
Db	159155	AGCTGTGTATGTAATGGTGAGACCCATAAACCATCTCTGTTTTCACCTTTCAGTAAG	159214	Db	160235	ATGAATATTACAACTCAGTGTGATTTTCAGAAATCCCTCTCTATATAATCAGCACATAAT	160294
QY	23101	TATTCATATAATATATAGCTATTAAACCTCTATTATATAAATAGGCTTTGGTAGATA	23160	QY	24181	TATGAAAACGTGTTTTCACATTTCAATCCCAATGCAGAGTGCAATATAATATCGAAAGA	24240
Db	159215	TATTCATATAATATATAGCTATTAAACCTCTATTATATAAATAGGCTTTGGTAGATA	159274	Db	160295	TATGAAAACGTGTTTTCACATTTCAATCCCAATGCAGAGTGCAATATAATATCGAAAGA	160354
QY	23161	ATACTGACCAACTATAGGCTGATATATGCTGTCTGAACATGTTTAAAGTAGGCTAGGCTT	23220	QY	24241	CAATTTATTTTAAAGTTTTAAATGAGGACTATCAGGATACTTTAACTTTAAATTTATGA	24300
Db	159275	ATACTGACCAACTATAGGCTGATATATGCTGTCTGAACATGTTTAAAGTAGGCTAGGCTT	159334	Db	160355	CAATTTATTTTAAAGTTTTAAATGAGGACTATCAGGATACTTTAACTTTAAATTTATGA	160414
QY	23221	AGCTAGAACTCAGTAGGCTATGCTATTGAATGGTGTGACTTTAACTATATTTTCCA	23280	QY	24301	GACACTGAATTTTGTGACTCCACATCTGGGTTTAAACATCTAAAGAATAAAACATTTACC	24360
Db	159335	AGCTAGAACTCAGTAGGCTATGCTATTGAATGGTGTGACTTTAACTATATTTTCCA	159394	Db	160415	GACACTGAATTTTGTGACTCCACATCTGGGTTTAAACATCTAAAGAATAAAACATTTACC	160474
QY	23281	ATTACAACTGTGTTTATTTGGGATGTAACCCATCAAAAGTTAAGAGCTCCATATTCAGS	23340	QY	24361	ACTTTGTTTTCACAAATTTAACTAAATCACAGCAAAAGATCTTAAATCAGACAAATTCCT	24420
Db	159395	ATTACAACTGTGTTTATTTGGGATGTAACCCATCAAAAGTTAAGAGCTCCATATTCAGS	159454	Db	160475	ACTTTGTTTTCACAAATTTAACTAAATCACAGCAAAAGATCTTAAATCAGACAAATTCCT	160534
QY	23341	TGCTTCTCTCTATTTGAACATAAAAGTTGTTGGAGGTAGAGGCTAACTATCTTTTAT	23400	QY	24421	GATTTTCAAGGTTTGAAGCATTTGTGAAGCAAGAGTGTAATGCAAACTTTACTGAGCAACT	24480
Db	159455	TGCTTCTCTCTATTTGAACATAAAAGTTGTTGGAGGTAGAGGCTAACTATCTTTTAT	159514	Db	160535	GATTTTCAAGGTTTGAAGCATTTGTGAAGCAAGAGTGTAATGCAAACTTTACTGAGCAACT	160594
QY	23401	CCCTCTCTCTAGTACTTTGCTTAAATGTAAGGACCAAAATGCACTCATTTCAAGCTCA	23460	QY	24481	ACTATGATTCACGACCTTTTGTGAGATGCTTTTACAAATTTCAAAATTTCAATTTAACTC	24540
Db	159515	CCCTCTCTCTAGTACTTTGCTTAAATGTAAGGACCAAAATGCACTCATTTCAAGCTCA	159574	Db	160595	ACTATGATTCACGACCTTTTGTGAGATGCTTTTACAAATTTCAAAATTTCAATTTAACTC	160654
QY	23461	CTTCTAAAACCATTTGACATTTCAAGGATTTAGGAGCAAGGTGCTGCAAGGAGGACCAACA	23520	QY	24541	AGCAAACTCTCATCTTATAGATATTACAAATTTCCCATTTGGATGATGAGAACTGAGTTGA	24600
Db	159575	CTTCTAAAACCATTTGACATTTCAAGGATTTAGGAGCAAGGTGCTGCAAGGAGGACCAACA	159634	Db	160655	AGCAAACTCTCATCTTATAGATATTACAAATTTCCCATTTGGATGATGAGAACTGAGTTGA	160714
QY	23521	TGCTCTTTTGGCAGATCCCTTTGCAAGAAATAGACACTCAATATTAATCTACCTGAATG	23580	QY	24601	GAGGACTTAAAGTGTGCTTAAAGCCACTGGAGCTAAAGTATGATGATGATGATGATGATG	24660
Db	159635	TGCTCTTTTGGCAGATCCCTTTGCAAGAAATAGACACTCAATATTAATCTACCTGAATG	159694	Db	160715	GAGGACTTAAAGTGTGCTTAAAGCCACTGGAGCTAAAGTATGATGATGATGATGATGATG	160774
QY	23581	AATCAGATAACCATGATTTTTCAGTTTAAATTTTATCAGAAAGGTGAACAAATTC	23640	QY	24661	CTGGAAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	24720
Db	159695	AATCAGATAACCATGATTTTTCAGTTTAAATTTTATCAGAAAGGTGAACAAATTC	159754	Db	160775	CTGGAAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	160834
QY	23641	AACTATCTTTCAGGAATGATAGATTTATTTAATCTTATATGTTGATGTTTGGATC	23700	QY	24721	AGTAACACCATCATAAAGCCATTTCTGAAACCTGGGAATTCATGACCTGGGCTGATGTA	24780
Db	159755	AACTATCTTTCAGGAATGATAGATTTATTTAATCTTATATGTTGATGTTTGGATC	159814	Db	160835	AGTAACACCATCATAAAGCCATTTCTGAAACCTGGGAATTCATGACCTGGGCTGATGTA	160894
QY	23701	TTATCTCAAGACTAGTCTAGGATGTTGGTGTAGTGGGAAAGTGTAGGTTAGAAATTAAGA	23760	QY	24781	TAAAGCATATCTAATAATGAAATTTTAAAAAACAAGTTAGGAGATGAAGGCTCTTA	24840
Db	159815	TTATCTCAAGACTAGTCTAGGATGTTGGTGTAGTGGGAAAGTGTAGGTTAGAAATTAAGA	159874	Db	160895	TAAAGCATATCTAATAATGAAATTTTAAAAAACAAGTTAGGAGATGAAGGCTCTTA	160954
QY	23761	ACTAGGATTTAGAACCATCTCTGCCAAGGATGAACCAAGATGATGATGATGATGATGATG	23820	QY	24841	AAATTTCTTCT	24900
Db	159875	ACTAGGATTTAGAACCATCTCTGCCAAGGATGAACCAAGATGATGATGATGATGATGATG	159934	Db	160955	AAATTTCTTCT	161014
QY	23821	AAGATCTGTGAATATAGGAGTGGACACATGTTAGGATGCTCTTGTGAGAGACTGGTT	23880	QY	24901	CTCAGAGCATGAGCTTTTGCAGCAACCAAGGCTTCTATGCTCATGATCTCTATTTTCT	24960
Db	159935	AAGATCTGTGAATATAGGAGTGGACACATGTTAGGATGCTCTTGTGAGAGACTGGTT	159994	Db	161015	CTCAGAGCATGAGCTTTTGCAGCAACCAAGGCTTCTATGCTCATGATCTCTATTTTCT	161074
QY	23881	CTCAGATGCAACATCAAGGCTGTAGGAACTTTGCTTTTCAATGGGAGACAGTGGC	23940	QY	24961	AGCTCTCAGAGAACTTCTGAAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT	25020
Db	159995	CTCAGATGCAACATCAAGGCTGTAGGAACTTTGCTTTTCAATGGGAGACAGTGGC	160054	Db	161075	AGCTCTCAGAGAACTTCTGAAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT	161134
QY	23941	ATAATCTGTTATGAAAGTGTAAACATTTCCCTTTAATGTTTGCAGCACACAGGTTTATGA	24000	QY	25021	GCTCTGCGCAAGAACTTCTTAAAGTAAATGAGTTTAAATGAGTTTAAATGAGTTTAAATG	25080
Db				Db	161135	GCTCTGCGCAAGAACTTCTTAAAGTAAATGAGTTTAAATGAGTTTAAATGAGTTTAAATG	161194

QY	25081	AATCCTACCTCAGTAGGTATGCCACATTTACTGAAGTGAATACACAGATCAAAAG	25140	QY	26161	CCCTCATAGACACACACATATGATAAACAATATGTTTTTATGATGCTTGTGCGC	26220
Db	161195	AATCCTACCTCAGTAGGTATGCCACATTTACTGAAGTGAATACACAGATCAAAAG	161254	Db	162275	CCCTCATAGACACACACATATGATAAACAATATGTTTTTATGATGCTTGTGCGC	162334
QY	25141	AAGGAAGTTTAAATCAGAAAGACCTTAAACACTAGAAGAGCTGAGATTCGTAAATGGTGA	25200	QY	26221	AAACAGAGTAGTGAGGAGCTAGATCTTACAATATCATATGAGTATTAACAGTGGCAA	26280
Db	161255	AAGGAAGTTTAAATCAGAAAGACCTTAAACACTAGAAGAGCTGAGATTCGTAAATGGTGA	161314	Db	162335	AAACAGAGTAGTGAGGAGCTAGATCTTACAATATCATATGAGTATTAACAGTGGCAA	162394
QY	25201	TTACTAAGGAATAGAGGCCATGCCACCTTGAACCTAAATACAAAAAGCCATGATCAGG	25260	QY	26281	AAGTCTCTAAAAGAAAAGCTTAGCAGAAAAACATCCCAATAGCAAAATAGTGTGAGAAA	26340
Db	161315	TTACTAAGGAATAGAGGCCATGCCACCTTGAACCTAAATACAAAAAGCCATGATCAGG	161374	Db	162395	AAGTCTCTAAAAGAAAAGCTTAGCAGAAAAACATCCCAATAGCAAAATAGTGTGAGAAA	162454
QY	25261	TGCTCTTCAAGTTGATTAACATCAGAGCTAACACTATCTCTTGGCAAGTGTATAGTCCATTC	25320	QY	26341	ATTTCTGGATAAATAGTATCAGAAAAGTTTGTAGTCTTGGAGATAATTTTGAACACTTTTA	26400
Db	161375	TGCTCTTCAAGTTGATTAACATCAGAGCTAACACTATCTCTTGGCAAGTGTATAGTCCATTC	161434	Db	162455	ATTTCTGGATAAATAGTATCAGAAAAGTTTGTAGTCTTGGAGATAATTTTGAACACTTTTA	162514
QY	25321	TCATACCTGAGATAAAGAAACACCCCAAGACTGGGTAGTTTATAAGAAAAAGAGTTTAAATG	25380	QY	26401	ATGAGTACACTGATTTATACAGATAATTAATAAGACATAATTTGGCAATATCTCTGTG	26460
Db	161435	TCATACCTGAGATAAAGAAACACCCCAAGACTGGGTAGTTTATAAGAAAAAGAGTTTAAATG	161494	Db	162515	ATGAGTACACTGATTTATACAGATAATTAATAAGACATAATTTGGCAATATCTCTGTG	162574
QY	25381	GCCTCACAGTTATGATTCCTGGAGGCTTAAGCAACTTACAACTATGCGCAGAGGCG	25440	QY	26461	AGGCTCTCCAGATTACTGATGTTTATCTAGAGCCTTATAGGGAAGACAGCAGACAAT	26520
Db	161495	GCCTCACAGTTATGATTCCTGGAGGCTTAAGCAACTTACAACTATGCGCAGAGGCG	161554	Db	162575	AGGCTCTCCAGATTACTGATGTTTATCTAGAGCCTTATAGGGAAGACAGCAGACAAT	162634
QY	25441	AAGGAAGCAAAAGCAGCTCTTACATGGTGGCAGGAGGAGAGCATGTGTCAAGTGTGA	25500	QY	26521	AATAGAAAATATCTTGGTCTGTGACAGAGTTTTCGAAGCAATTTCAAAATATACAGTAGCT	26580
Db	161555	AAGGAAGCAAAAGCAGCTCTTACATGGTGGCAGGAGGAGAGCATGTGTCAAGTGTGA	161614	Db	162635	AATAGAAAATATCTTGGTCTGTGACAGAGTTTTCGAAGCAATTTCAAAATATACAGTAGCT	162694
QY	25501	GGGGAACCTGCCCTTTTAAATCATCAGATCTGTGGCACTCATCTATCACAGAAT	25560	QY	26581	ATCATTTATGAGGCTGTAGATCTCTTCAATACCTTAATCCCTAACCAAAATTTGCAAA	26640
Db	161615	GGGGAACCTGCCCTTTTAAATCATCAGATCTGTGGCACTCATCTATCACAGAAT	161674	Db	162695	ATCATTTATGAGGCTGTAGATCTCTTCAATACCTTAATCCCTAACCAAAATTTGCAAA	162754
QY	25561	AGCATGGGAAACCATCCCATGATTCAATTTATCTCCATCTGTGTTCTCCCTTCACATG	25620	QY	26641	GTGCTTATAAATAGAGGCCATTTTACAAAGAGAAGAAAATAGAGATCAGGGGTCTGTAG	26700
Db	161675	AGCATGGGAAACCATCCCATGATTCAATTTATCTCCATCTGTGTTCTCCCTTCACATG	161734	Db	162755	GTGCTTATAAATAGAGGCCATTTTACAAAGAGAAGAAAATAGAGATCAGGGGTCTGTAG	162814
QY	25621	TGGGATTTATGGGATTTGGGATTTGCAATTCAGATGAGATTTGGTGGGACACAAAT	25680	QY	26701	TGACTTCTCCAAGGCCACTGCTACTGATTTTAGGATTTTAGGATTTAGATTTTATTAACAAGT	26760
Db	161735	TGGGATTTATGGGATTTGGGATTTGCAATTCAGATGAGATTTGGTGGGACACAAAT	161794	Db	162815	TGACTTCTCCAAGGCCACTGCTACTGATTTTAGGATTTTAGGATTTAGATTTTATTAACAAGT	162874
QY	25681	GCATCACTATATTACAGAGTAAGACACTCAGTGGATTTGGATCTCTCAGCAGCAGCAGG	25740	QY	26761	TAGTTTGACTCTCAAGTCCATGCTCTTCCATTCGCAAGTCTCTCTCTTCTTCTGCTCTAT	26820
Db	161795	GCATCACTATATTACAGAGTAAGACACTCAGTGGATTTGGATCTCTCAGCAGCAGCAGG	161854	Db	162875	TAGTTTGACTCTCAAGTCCATGCTCTTCCATTCGCAAGTCTCTCTCTTCTTCTGCTCTAT	162934
QY	25741	CCTACAAGCATATAGCTCTAGGAGCAGTGTAGTCTCTTCACTTAACTTAACTTAACTTAA	25800	QY	26821	TTCTATTAAATTTATGCCCCAACAAATTTTAAATTTGATATAATAAATAAATAAATAAATAA	26880
Db	161855	CCTACAAGCATATAGCTCTAGGAGCAGTGTAGTCTCTTCACTTAACTTAACTTAACTTAA	161914	Db	162935	TTCTATTAAATTTATGCCCCAACAAATTTTAAATTTGATATAATAAATAAATAAATAAATAA	162994
QY	25801	AGGAAACAATCCCAATAAATTTTCCAAATGCTTCCACAGAAAAAATTTAGCAGCAAAAC	25860	QY	26881	GGTACCAATATACACATGTTTCAGGAACTCAATGAAGCTAACCATCTTTTCAATAATA	26940
Db	161915	AGGAAACAATCCCAATAAATTTTCCAAATGCTTCCACAGAAAAAATTTAGCAGCAAAAC	161974	Db	162995	GGTACCAATATACACATGTTTCAGGAACTCAATGAAGCTAACCATCTTTTCAATAATA	163054
QY	25861	ACAAGGAACACACATTTCTTTTAAACAGAGTAATGAGTGGGAAATTTGCAATTTGTC	25920	QY	26941	GAACCTATTATTAACAATAATGTRATATTATTAAGCAACACAGTATTATTATTAATGCTTA	27000
Db	161975	ACAAGGAACACACATTTCTTTTAAACAGAGTAATGAGTGGGAAATTTGCAATTTGTC	162034	Db	163055	GAACCTATTATTAACAATAATGTRATATTATTAAGCAACACAGTATTATTATTAATGCTTA	163114
QY	25921	ATCCGACGCTAAAGTTTACCTATGCTTCCACTGTCAACTGGATTTTCTTATTTGATTT	25980	QY	27001	TTATCTACTGATGTACCAGTACCTCTTAAATTTTACAGAGATGTAGTTTACAGATATCTGA	27060
Db	162035	ATCCGACGCTAAAGTTTACCTATGCTTCCACTGTCAACTGGATTTTCTTATTTGATTT	162094	Db	163115	TTATCTACTGATGTACCAGTACCTCTTAAATTTTACAGAGATGTAGTTTACAGATATCTGA	163174
QY	25981	GCATTTGAATGACATGCTTAGATGAGGGAATAAATTTGATAATGAGGCTGGGTTAGGA	26040	QY	27061	AGACTGATGATCTGACATCATCTGCTGGGCAACAGCTTTTGGCAAAATCTTCAACC	27120
Db	162095	GCATTTGAATGACATGCTTAGATGAGGGAATAAATTTGATAATGAGGCTGGGTTAGGA	162154	Db	163175	AGACTGATGATCTGACATCATCTGCTGGGCAACAGCTTTTGGCAAAATCTTCAACC	163234
QY	26041	TATCCACAAGACGACAACTGCGTCTAGGATGAAGCAGAGGTGGCAGCAGCAGGA	26100	QY	27121	CAAGTATCAAAATAGCAGACAGAAAAATTCAGAGCACTAGTTTCTAAAATATGCTTCAAT	27180
Db	162155	TATCCACAAGACGACAACTGCGTCTAGGATGAAGCAGAGGTGGCAGCAGCAGGA	162214	Db	163235	CAAGTATCAAAATAGCAGACAGAAAAATTCAGAGCACTAGTTTCTAAAATATGCTTCAAT	163294
QY	26101	GAAAAACAACTGAAAGTTGCCCCACTGCTGAGATTTTCTTAAATAATTTTCAATGTGTG	26160	QY	27181	ATGTTAATGCTCTCTGAAATAATTTCTTACATTTGAAATTCATTTTGAATAATCAAACTT	27240
Db	162215	GAAAAACAACTGAAAGTTGCCCCACTGCTGAGATTTTCTTAAATAATTTTCAATGTGTG	162274	Db	163295	ATGTTAATGCTCTCTGAAATAATTTCTTACATTTGAAATTCATTTTGAATAATCAAACTT	163354
				QY	27241	GTGCTCTCTCTTTAGCATGCGGCAATGACAAAGAACAGCAATAATGATATAAATTT	27300

Db	164435	ATACATTGTCCTTAAATTCATAGGTATATGTTTTTCTGTTTTTGTGTTTTTCTGTTTTTAAATTT	164494
Qy	28381	TTATGATTATTATACCTTTAAGTTTATAGAGTACATATGCACAATGTGCAGGTTTGTACAT	28440
Db	164495	TTATGATTATTATACCTTTAAGTTTATAGAGTACATATGCACAATGTGCAGGTTTGTACAT	164554
Qy	28441	ATGTATACATGTGCCATGTGGTGTGCTGCACCCATTAACCTGTCTCATTTTAAACATTTAGGTA	28500
Db	164555	ATGTATACATGTGCCATGTGGTGTGCTGCACCCATTAACCTGTCTCATTTTAAACATTTAGGTA	164614
Qy	28501	TATCTCCTAATGTATCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT	28560
Db	164615	TATCTCCTAATGTATCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT	164674
Qy	28561	GTTCCTCCTCCTGTGCTCCTGTCTCATTTTGTTCAAATTTCCCACTTATGAGTGAGAACAT	28620
Db	164675	GTTCCTCCTCCTGTGCTCCTGTCTCATTTTGTTCAAATTTCCCACTTATGAGTGAGAACAT	164734
Qy	28621	CGCGTGTGTTTTTGTGCTCCTTGTGATAGTTTGTCTGCTGAGAAATGATGGTTCCAGCTTCAT	28680
Db	164735	CGCGTGTGTTTTTGTGCTCCTTGTGATAGTTTGTCTGCTGAGAAATGATGGTTCCAGCTTCAT	164794
Qy	28681	CCATGTCCTTACAAAGGACACGAACATCATCATTTTTTATGGCTGTCATAGTATTTCCATGGT	28740
Db	164795	CCATGTCCTTACAAAGGACACGAACATCATCATTTTTTATGGCTGTCATAGTATTTCCATGGT	164854
Qy	28741	GTATATGTGTCACATTTTCTTAATCCAGTCTATCTGTTTGGACATTTAGTGTGGTTCCA	28800
Db	164855	GTATATGTGTCACATTTTCTTAATCCAGTCTATCTGTTTGGACATTTAGTGTGGTTCCA	164914
Qy	28801	AGTCTTTTGTGTTGTGTAATAGTCTGCTATAAACATACATGCTTGTGCTTTTATPAGCA	28860
Db	164915	AGTCTTTTGTGTTGTGTAATAGTCTGCTATAAACATACATGCTTGTGCTTTTATPAGCA	164974
Qy	28861	GCATGATTATATCTCCTTGGGTATATACCACGTAATGGATGGCTGGCTCAAAATGGTAT	28920
Db	164975	GCATGATTATATCTCCTTGGGTATATACCACGTAATGGATGGCTGGCTCAAAATGGTAT	165034
Qy	28921	TTCTAGTCTTAGATCCCTGAGGAATCACACACTGACTTCCACAAATGGTTGAACATAGTTC	28980
Db	165035	TTCTAGTCTTAGATCCCTGAGGAATCACACACTGACTTCCACAAATGGTTGAACATAGTTC	165094
Qy	28981	ACAGTCCCAACAAACAGTGTAAAAGTGTCTCTATTTCTCCACATTTCTCTCCAGCACCTGTT	29040
Db	165095	ACAGTCCCAACAAACAGTGTAAAAGTGTCTCTATTTCTCCACATTTCTCTCCAGCACCTGTT	165154
Qy	29041	GTATCTCTGACTTTTAAATGATTGCCATCTCTAACTGGTGTGAGATGTATCTCATTTGCTGT	29100
Db	165155	GTATCTCTGACTTTTAAATGATTGCCATCTCTAACTGGTGTGAGATGTATCTCATTTGCTGT	165214
Qy	29101	TTTTCATTTTGCATTTCTCTGATGCCAGTGTATGATAGTATTTTTCATGTGTTTTTGTGGC	29160
Db	165215	TTTTCATTTTGCATTTCTCTGATGCCAGTGTATGATAGTATTTTTCATGTGTTTTTGTGGC	165274
Qy	29161	TGCATAAATGCCTTCTTTTGTGAGAAGTGTCTGTTTCATATCCTTCCACCACTTTTGTGATGGG	29220
Db	165275	TGCATAAATGCCTTCTTTTGTGAGAAGTGTCTGTTTCATATCCTTCCACCACTTTTGTGATGGG	165334
Qy	29221	GTTCCTTTGTTTTTTTCTTGTGTAATTTGTTTGTAGTTCATTTGTAGATTTCTGATATTAGCCC	29280
Db	165335	GTTCCTTTGTTTTTTTCTTGTGTAATTTGTTTGTAGTTCATTTGTAGATTTCTGATATTAGCCC	165394
Qy	29281	TTTCTCAAAATGAGTAGGTTCGCAAAAATTTTCTCCCATCTCTGTAAGTTGCTGTTCACCTCT	29340
Db	165395	TTTCTCAAAATGAGTAGGTTCGCAAAAATTTTCTCCCATCTCTGTAAGTTGCTGTTCACCTCT	165454
Qy	29341	GATGGTAGTTTCTTTTGTCTGTGCAGAGCTCTTTTAGTTTTAAATTTAGATCCCATTTGTCAAT	29400
Db	165455	GATGGTAGTTTCTTTTGTCTGTGCAGAGCTCTTTTAGTTTTAAATTTAGATCCCATTTGTCAAT	165514
Qy	29401	TTTGGCTTTTGTGTCCTGCTTTTGGTGTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTTAAAT	29460
Db	165515	TTTGGCTTTTGTGTCCTGCTTTTGGTGTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTTAAAT	165574



QY 1081 TGCTGTTATATCTAAATCTTTGGTTGAAGTAAACATGTTGCCCTGGAGTTGCTGGCAAG 11140  
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QY 1141 ATGGCCGAACAGAAAGCTCTGGTCTGCAGTTCAGAGGAGATCAATGCAAGAGCGGG 1200  
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Db 41003 ATGGCCGAACAGAAAGCTCTGGTCTGCAGTTCAGAGGAGATCAATGCAAGAGCGGG 41062  
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QY 1201 TGATTTCTCCATTCACCACTGAGTACCCAGTTTCATCTCACTGGGACTGGTTAGACATTG 1260  
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Db 41063 TGAATTTCTCCATTCACCACTGAGTACCCAGTTTCATCTCACTGGGACTGGTTAGACATTG 41122  
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QY 1261 GGTGCAGCCACGAAGAGTGAAGTGAAGCAGGGTGGGGTCTCCCTCAGCGCGCAAGTGC 1320  
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QY 1321 AAGGGGTGGGGATCTCTTCCCTCCAGCAAGGAGCCATGAGAGACTGTACCAAGGAG 1380  
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QY 1381 GAATGTTGCACTCTAGTCCAGATAGTCCACTTTTCCCATAGTCTTTGCCAACTGGCAGAC 1440  
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Db 41243 GAATGTTGCACTCTAGTCCAGATAGTCCACTTTTCCCATAGTCTTTGCCAACTGGCAGAC 41302  
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QY 1501 GGCATTTGGACAGACACCGAGTGTAGCCGAGCAGTATATTTTCATACCCCTAGTGGCGC 1560  
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Db 41363 GGCATTTGGACAGACACCGAGTGTAGCCGAGCAGTATATTTTCATACCCCTAGTGGCGC 41422  
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QY 1621 GTCCCACTCCCTAGGAGCCAGCTAGCTAGATCCACTGGCTTGAATTTCTCCTGCCAGC 1680  
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QY 1681 ACAGAGTCTGAGATTGACCTGGATGCTTGGTGGTGGAGGGGCGTCTGCCAT 1740  
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Db 41963 CCCATGTATCTCTGACTGGGAGACATCTCCATTTAGGGGCCATAGACATTTTCATACAGG 42022  
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QY 2636 AAGCAAGAACTTCATGAAGCATACACAAGCTTCAATAGCAAACTCGATCAAGCAGAGA 2695  
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QY 2696 AAGATATCAGTATTGATGATCAAAATTAATAAGAAAGAGTGAAGACAGAAATACAGA 2755  
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Db 43043 CAACCCAGAAATTTTCATATCCAGCCAAACCAAGCTTCTTAAGTGAAGGAGAAATAATTC 43102  
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QY 3236 TCTACAGAGAAAGCAAAATGCTGACAGATTTTGTGACCCAGCGCTGCCTTACAAGAGCT 3295  
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Db	43103	 TCTACAGAGAACCAAAATGCTGACAGATTTTGTGCACACACAGGCCTGCCTTACAAGAGCT	43162
Qy	3296	CCTGAAGGAAGCACCAACATGGAAAGGAACAACCTGGTACCAGGCACCTGCAAAAACATCCC 	3355
Db	43163	CCTGAAGGAAGCACCAACATGGAAAGGAACAACCTGGTACCAGGCACCTGCAAAAACATCCC 	43222
Qy	3356	AAATTGTAAGACACCATTTGATGCTATGAAGAAAGTGATCACTAACTAACGGGGCAAAATAACCA 	3415
Db	43223	AAATTGTAAGACACCATTTGATGCTATGAAGAAAGTGATCACTAACTAACGGGGCAAAATAACCA 	43282
Qy	3416	GCTAGTGTCATAATGGCAGGATCAAAATTCACACATATAATATTAACCTTTAAATGTAAT 	3475
Db	43283	GCTAGTGTCATAATGGCAGGATCAAAATTCACACATATAATATTAACCTTTAAATGTAAT 	43342
Qy	3476	GGGCTAAATTCCTCCAAATTAAGACACAGACTGGCAAAATGGATAAAGAGTCAAGACCCA 	3535
Db	43343	GGGCTAAATTCCTCCAAATTAAGACACAGACTGGCAAAATGGATAAAGAGTCAAGACCCA 	43402
Qy	3536	TCAGTGTGCTGATTTACAGGAGGCCATCTCACATGAAAGACACACATAGGCTCAAAATA 	3595
Db	43403	TCAGTGTGCTGATTTACAGGAGGCCATCTCACATGAAAGACACACATAGGCTCAAAATA 	43462
Qy	3596	AAGGGATGGAGGAAGATTTACCAAGTAAATGGAATAACAAAAAAGAGAGGGTTGCA 	3655
Db	43463	AAGGGATGGAGGAAGATTTACCAAGTAAATGGAATAACAAAAAAGAGAGGGTTGCA 	43522
Qy	3656	ATCCTAGTCTCTGATAAACAGACTTTAAACCAACAAAGATCAAAAGAGACAAAGAAGGC 	3715
Db	43523	ATCCTAGTCTCTGATAAACAGACTTTAAACCAACAAAGATCAAAAGAGACAAAGAAGGC 	43582
Qy	3716	CATTACATAATGGTAAAGGCATCAATGGAAACAAGAAGAGCTAACTATCCTAAATATACAT 	3775
Db	43583	CATTACATAATGGTAAAGGCATCAATGGAAACAAGAAGAGCTAACTATCCTAAATATACAT 	43642
Qy	3776	GCACCAATACAGAGCACCAGATTCATATAAGCAAGTTCTTTAGAGACCTTACAAAGAGAC 	3835
Db	43643	GCACCAATACAGAGCACCAGATTCATATAAGCAAGTTCTTTAGAGACCTTACAAAGAGAC 	43702
Qy	3836	TTTGACTCCACACAATAATAGTGGAGTCTAAATAATTAATAGACACTTTAACACCCCA 	3895
Db	43703	TTTGACTCCACACAATAATAGTGGAGTCTAAATAATTAATAGACACTTTAACACCCCA 	43762
Qy	3896	CTGCCAATATTAGGCAGATCAATGAGACAGAAAAATTAACAAGGATATCCAGGAGTTGAAC 	3955
Db	43763	CTGCCAATATTAGGCAGATCAATGAGACAGAAAAATTAACAAGGATATCCAGGAGTTGAAC 	43822
Qy	3956	TGAGCTCTGGACCAAGCGGACCTTAATAGATATCTACAGAACTCCCCACCCCAAAATCAACA 	4015
Db	43823	TGAGCTCTGGACCAAGCGGACCTTAATAGATATCTACAGAACTCCCCACCCCAAAATCAACA 	43882
Qy	4016	GAATATACACTCTCTCAGCATCACATTAACACCTATTTTAAATTTGACCATGTAATTTTA 	4075
Db	43883	GAATATACACTCTCTCAGCATCACATTAACACCTATTTTAAATTTGACCATGTAATTTTA 	43942
Qy	4076	AGTAAACACTCTCTCAGCAAAATGCAAAAGAACAGAAATCCTTACAAACAGTCTCTCAGAC 	4135
Db	43943	AGTAAACACTCTCTCAGCAAAATGCAAAAGAACAGAAATCCTTACAAACAGTCTCTCAGAC 	44002
Qy	4136	TACAGTGCAATCTATTTAGAACTCAGAAATTAAGAAACTCAGTCAAAATCAGCAACTACA 	4195
Db	44003	TACAGTGCAATCTATTTAGAACTCAGAAATTAAGAAACTCAGTCAAAATCAGCAACTACA 	44062
Qy	4196	TGGAACTGAACAACTGCTCTGATGATGACTACTGGGTAATTAACAAATGAAGGCAAA 	4255
Db	44063	TGGAACTGAACAACTGCTCTGATGATGACTACTGGGTAATTAACAAATGAAGGCAAA 	44122
Qy	4256	ATAAGATGTTCTTTGAACCAATGAGACAAAGACACAATGTACCAGAAATCTCTGGGCG 	4315
Db	44123	ATAAGATGTTCTTTGAACCAATGAGACAAAGACACAATGTACCAGAAATCTCTGGGCG 	44182
Qy	4316	ATATTTAAAGCAGTGTGTAGAGGGAATTTATAGCACTAGATGCGCTTACAGAGAAAGCAG 	4375



QY	5456	CAGTGACACACAAAAAGAGAAATTTTCAGGCCCATATCCCTGATGAACATTTGATGTGAA	5515	QY	6535	AACCAAACTGCATGTTACTGGTACCAAAAACAGATATATAGACCAATGGAACAGACAGA	6594
Db	45323	CAGTGACACACAAAAAGAGAAATTTTCAGGCCCATATCCCTGATGAACATTTGATGTGAA	45382	Db	46403	AACCAAACTGCATGTTACTGGTACCAAAAACAGATATATAGACCAATGGAACAGACAGA	46462
QY	5516	AATCCTCAATAAATACTGGCAACCAAAATCCAGCAGCAGCATCAAAAAGCTTATCTACCA	5575	QY	6595	GACCTCAGAAATTTACACTGCAATCTACATCCATCTGATCTTTGACAAACCTGACAAAAC	6654
Db	45383	AATCCTCAATAAATACTGGCAACCAAAATCCAGCAGCAGCATCAAAAAGCTTATCTACCA	45442	Db	46463	GACCTCAGAAATTTACACTGCAATCTACATCCATCTGATCTTTGACAAACCTGACAAAAC	46522
QY	5576	TGATCAAGTTGGGCTCATCCCTGGGATGCAAGCTGTTCAAAATATGCAAAATCAATAAA	5635	QY	6655	AAGCAATGGAAAAAGGATTCCTTATTTAATAAATGGTGTGGAAAAACTGGCTAGCCATA	6714
Db	45443	TGATCAAGTTGGGCTCATCCCTGGGATGCAAGCTGTTCAAAATATGCAAAATCAATAAA	45502	Db	46523	ARGCAATGGAAAAAGGATTCCTTATTTAATAAATGGTGTGGAAAAACTGGCTAGCCATA	46582
QY	5636	TGTAGGCCATCACATAACAGAACCAATGACAAAAACCATGATTTCTCAATAGATGC	5695	QY	6715	TGCAGAAAGCTGAAACTGGATCCCTTCCCTTACACCTTTATACAAAAGTTAACTCAAGATGA	6774
Db	45503	TGTAGGCCATCACATAACAGAACCAATGACAAAAACCATGATTTCTCAATAGATGC	45562	Db	46583	TGCAGAAAGCTGAAACTGGATCCCTTCCCTTACACCTTTATACAAAAGTTAACTCAAGATGA	46642
QY	5696	AGAAAGCCCTTTGTCAAAATTCACAGCCCTTCATGCTAAAAATTCCTAGTAACTAGG	5755	QY	6775	ATTAAAGACCTTTAATAAGACATATAAACCATATAAAACCCAGAGAAACCTTAGGCAATA	6834
Db	45563	AGAAAGCCCTTTGTCAAAATTCACAGCCCTTCATGCTAAAAATTCCTAGTAACTAGG	45622	Db	46643	ATTAAAGACCTTTAATAAGACATATAAAACCATATAAAACCCAGAGAAACCTTAGGCAATA	46702
QY	5756	TATCGATGGAATGTATCTCAAAATAATAAGAGCTATTTTACAAAACCCAGGCAATATC	5815	QY	6835	CCATTGAGGATATGGACATGGCAAGACTTTCATGACTAAAAACACCAAAAGCAATGCAA	6894
Db	45623	TATCGATGGAATGTATCTCAAAATAATAAGAGCTATTTTACAAAACCCAGGCAATATC	45682	Db	46703	CCATTGAGGATATGGACATGGCAAGACTTTCATGACTAAAAACCAAAAGCAATGCAA	46762
QY	5816	ATACTGAATGGCAAAAACCTGGAGCATTCCTCTTTGAGAACTGGCACAAGCAGGATGC	5875	QY	6895	CAAAAGCCAAAATAGACAAAGTGGGATCTGATTTAACTATATAGAGCTTCTGCACACAAAA	6954
Db	45683	ATACTGAATGGCAAAAACCTGGAGCATTCCTCTTTGAGAACTGGCACAAGCAGGATGC	45742	Db	46763	CAAAAGCCAAAATAGACAAAGTGGGATCTGATTTAACTATATAGAGCTTCTGCACACAAAA	46822
QY	5876	CTCTCTCACCACCTTATTCAGATPACTATTTGGAAGTTCTGGCCAGGGCAATCAGGCAA	5935	QY	6955	AAAACCTCATCAGAGTGAACAGCAACCTTACAGAAATGGGAGAAATTTTTCGAATCTAT	7014
Db	45743	CTCTCTCACCACCTTATTCAGATPACTATTTGGAAGTTCTGGCCAGGGCAATCAGGCAA	45802	Db	46823	AAAACCTCATCAGAGTGAACAGCAACCTTACAGAAATGGGAGAAATTTTTCGAATCTAT	46882
QY	5936	TAGAAAGAAATAAGGGTATTCAAATAGAAAGAGAGAACTATATTTGCTCTGTTTGA	5995	QY	7015	CGATCTCACAAAGCTTAATATCCAGAGATCTACGAAGAATTTAAACAAATTTTACAGAAA	7074
Db	45803	TAGAAAGAAATAAGGGTATTCAAATAGAAAGAGAGAACTATATTTGCTCTGTTTGA	45862	Db	46883	CGATCTCACAAAGCTTAATATCCAGAGATCTACGAAGAATTTAAACAAATTTTACAGAAA	46941
QY	5996	GATGACATGTTTGTATTTTAGAAAAACCCATCGTCTCAGGCCAAAAACCTCCCTTAAGCTG	6055	QY	7075	AAAACAAACCCCGTCAAAATATGGCAAAAGGATATGAGCAGACACTTCTCAAAAAGAGACA	7134
Db	45863	GATGACATGTTTGTATTTTAGAAAAACCCATCGTCTCAGGCCAAAAACCTCCCTTAAGCTG	45922	Db	46942	AAAACAAACCCCGTCAAAATATGGCAAAAGGATATGAGCAGACACTTCTCAAAAAGAGACA	47001
QY	6056	ATAGCAACCTCAGCAAGTCTCAGGACACAAAATCAATGTGCGAATAATCAGACATTC	6115	QY	7135	TTTATGAGCCCAACAAACATATGAAAAAACCTCATCATCTGTTGTTAGAAATGC	7194
Db	45923	ATAGCAACCTCAGCAAGTCTCAGGACACAAAATCAATGTGCGAATAATCAGACATTC	45982	Db	47002	TTTATGAGCCCAACAAACATATGAAAAAACCTCATCATCTGTTGTTAGAAATGC	47061
QY	6116	TTATACGCCAATATACACAAACAGAGAGCCAAATCATGATGAACTCTCATTCACAAAT	6175	QY	7195	AAAACAAACCAACAGTGCACATACCCTCATCTGCTAGTTAGAAATGCTGATCACTAAAAAT	7254
Db	45983	TTATACGCCAATATACACAAACAGAGAGCCAAATCATGATGAACTCTCATTCACAAAT	46042	Db	47062	AAAACAAACCAACAGTGCACATACCCTCATCTGCTAGTTAGAAATGCTGATCACTAAAAAT	47121
QY	6176	GCTACAAAGAGATAAATAACCTAGGAATACAACTTACAAAGGACACGCTAGGAATCTTC	6235	QY	7255	CAGAAACAAACAAATGCTGGAGAGGATGTGGAGAAATAGGAACACTTTTCCACTGTTGGT	7314
Db	46043	GCTACAAAGAGATAAATAACCTAGGAATACAACTTACAAAGGACACGCTAGGAATCTTC	46102	Db	47122	CAGAAACAAACAAATGCTGGAGAGGATGTGGAGAAATAGGAACACTTTTCCACTGTTGGT	47181
QY	6236	AAGGAGAACTACAAACCACTGATCAAGGAATATAGAGAGGACACAAACAAATGGAANAAC	6295	QY	7315	GGGAATGTAATTTAGTTTCAACCATTTGGAGAGAGGATGTGGAGAAATAGGAACACTTTT	7374
Db	46103	AAGGAGAACTACAAACCACTGATCAAGGAATATAGAGAGGACACAAACAAATGGAANAAC	46162	Db	47182	GGGAATGTAATTTAGTTTCAACCATTTGGAGAGAGGATGTGGAGAAATAGGAACACTTTT	47241
QY	6296	ATTCATGCTCACAGATAGTAAGAAATCATGAAAT - GCCATCTGCCCCCAAGTAAATAT	6354	QY	7375	AACCAAGAAATATCTTTGACCCAGCAATCCCATTTACTGAGTATATACCCAAAGGAATATA	7434
Db	46163	ATTCATGCTCACAGATAGTAAGAAATCATGAAATGCCCATCTGCCCCCAAGTAAATAT	46222	Db	47242	AACCAAGAAATATCTTTGACCCAGCAATCCCATTTACTGAGTATATACCCAAAGGAATATA	47301
QY	6355	AGATTGAGTGTACCCCCCATCAAGCTACCATTTGACTTTCTTACAGAAATTTGAAAAACA	6414	QY	7435	AATCATTTCTATTATAAGACACATGACACATATGTTTATTTGACGACTGATCATCAATAG	7494
Db	46223	AGATTGAGTGTACCCCCCATCAAGCTACCATTTGACTTTCTTACAGAAATTTGAAAAACA	46282	Db	47302	AATCATTTCTATTATAAGACACATGACACATATGTTTATTTGACGACTGATCATCAATAG	47361
QY	6415	ACTTTAAATTTTCATATGGAACCAAAAAAGAGCCACAGAGCCAGCAATCTTAAGCAA	6474	QY	7495	CAAGACTTTGGAACCAACCCCAATGTCATCAGTATAGACTGATGATTAAGAAACATGCG	7554
Db	46283	ACTTTAAATTTTCATATGGAACCAAAAAAGAGCCACAGAGCCAGCAATCTTAAGCAA	46342	Db	47362	CAAGACTTTGGAACCAACCCCAATGTCATCAGTATAGACTGATGATTAAGAAACATGCG	47421
QY	6475	AAAGAACAAAGCTGGAGGTATCATGCTACCTGACTTAAACTATATACATAGGCTACAGT	6534	QY	7555	ACATATACACCATGAAATATCTATGACGCCATATAAAAGGATGAGTTCTGCTTTGCGAGA	7614
Db	46343	AAAGAACAAAGCTGGAGGTATCATGCTACCTGACTTAAACTATATACATAGGCTACAGT	46402	Db	47422	ACATATACACCATGAAATATCTATGACGCCATATAAAAGGATGAGTTCTGCTTTGCGAGA	47481
				QY	7615	GATATGATGAAGCTGGAACCAACCATTTCTCAGCAAACTAACACAGAACAGAAACCAA	7674

Db	47482	GATATGATGAAGCTGGAACCATCATCTCAGCAAACTAACACAAAGAACAGAAAACCCA	47541	Db	48562	CTTGAACTTTTGTCTAGTGAAGTTAGATGCCTGGAGTCCCTCCACTCATGCATCAC	48621
QY	7675	ACACCACATGTTCTCACTTGTAGTGGAGTTCGAACAATGAGAAGACATGGACACAGGGA	7734	QY	8755	GGTCTGCACATCCCTTTTCATTTAGAAATTTGGCATGCTCTTCATAGACGGTCCAGTGAG	8814
Db	47542	ACACCACATGTTCTCACTTGTAGTGGAGTTCGAACAATGAGAAGACATGGACACAGGGA	47601	Db	48622	GGTCTGCACATCCCTTTTCATTTAGAAATTTGGCATGCTCTTCATAGACGGTCCAGTGAG	48681
QY	7735	GGGGAACATCACACACAGGTCCTGTTTGTGGTGGGACTAGGGAAGGATAGCATTA	7794	QY	8815	GCAGGGAATPAATCACTGCAATTTGTTTAATGTTCAATCAAGTTAGGGCACTCTGCTGATG	8874
Db	47602	GGGGAACATCACACACAGGTCCTGTTTGTGGTGGGACTAGGGAAGGATAGCATTA	47661	Db	48682	GCAGGGAATPAATCACTGCAATTTGTTTAATGTTCAATCAAGTTAGGGCACTCTGCTGATG	48741
QY	7795	GGAGAATACCTAATGATGACGCGGTTGATGGGTGCAGACAGCCACCATGGCACATGT	7854	QY	8875	CAGAAATGGAAGATGGAGATCTGTTTGTGAAAGAACTTCAAAAGACTTGCAGTACAAAGT	8934
Db	47662	GGAGAATACCTAATGATGACGCGGTTGATGGGTGCAGACAGCCACCATGGCACATGT	47721	Db	48742	CAGAAATGGAAGATGGAGATCTGTTTGTGAAAGAACTTCAAAAGACTTGCAGTACAAAGT	48801
QY	7855	ATACCTATGTAACAAACCTGCACATTCGCACATGTACCCCAACCTTAAAGTATTAAAA	7914	QY	8935	TGGCAGGGGTGGAGGAAGAAATACCTTAAGAAAGTCTTTTAGGGAGACAAAGTGCAGA	8994
Db	47722	ATACCTATGTAACAAACCTGCACATTCGCACATGTACCCCAACCTTAAAGTATTAAAA	47781	Db	48802	TGGCAGGGGTGGAGGAAGAAATACCTTAAGAAAGTCTTTTAGGGAGACAAAGTGCAGA	48861
QY	7915	AAAAACACACACATGTTGCCCTGATGAAGTTCATTAGTGGCCATPAATAAGTAAAAATG	7974	QY	8995	AATTTTGATATTGGGTAAAGCTAGTCCAAAGCCAGTTTGTAGTAGTTCATTATATCAT	9054
Db	47782	AAAAACACACACATGTTGCCCTGATGAAGTTCATTAGTGGCCATPAATAAGTAAAAATG	47841	Db	48862	AATTTTGATATTGGGTAAAGCTAGTCCAAAGCCAGTTTGTAGTAGTTCATTATATCAT	48921
QY	7975	TGTTTTATGTTTATATATTGTTAAACATATAATATCCTTTACCATTAAAAACAAATCA	8034	QY	9055	CTCCTGCAATTTCTATTTGCACCTTACAAATAGGTACCTTGGAGGGTGGGGTTGGACTCC	9114
Db	47842	TGTTTTATGTTTATATATTGTTAAACATATAATATCCTTTACCATTAAAAACAAATCA	47901	Db	48922	CTCCTGCAATTTCTATTTGCACCTTACAAATAGGTACCTTGGAGGGTGGGGTTGGACTCC	48981
QY	8035	GGTTCCACATAAATCTTCTATTAATACCTGTGTATCAATACAGCATTTCTTAAATCA	8094	QY	9115	CATAGCTTGGCAAGAAATTTCTCCAAAGTGAATTAATTCGTATTTTCCAAAGACTATCTGG	9174
Db	47902	GGTTCCACATAAATCTTCTATTAATACCTGTGTATCAATACAGCATTTCTTAAATCA	47961	Db	48982	CATAGCTTGGCAAGAAATTTCTCCAAAGTGAATTAATTCGTATTTTCCAAAGACTATCTGG	49041
QY	8095	ATAAGTATATCATTAATTTTAAATTCATAAAGTTAAACATAATTTCTTAAATTAGTAGT	8154	QY	9175	CCTGTAAAAGAGATTGTAGAACTAGGGATGAGGAGGAGGAAATTAATTTCTAAAGAACT	9234
Db	47962	ATAAGTATATCATTAATTTTAAATTCATAAAGTTAAACATAATTTCTTAAATTAGTAGT	48021	Db	49042	CCTGTAAAAGAGATTGTAGAACTAGGGATGAGGAGGAGGAAATTAATTTCTAAAGAACT	49101
QY	8155	TAAATAGAGCCAAACCTTCTCCCTGCAGTGGCCCTTCAATTTAGTGAATATATAGCTATT	8214	QY	9235	GAGCATATGATTAATATTCCTTGTGTTAAAGAGACTGTTATCAAGCCCTAAATAATTGTG	9294
Db	48022	TAAATAGAGCCAAACCTTCTCCCTGCAGTGGCCCTTCAATTTAGTGAATATATAGCTATT	48081	Db	49102	GAGCATATGATTAATATTCCTTGTGTTAAAGAGACTGTTATCAAGCCCTAAATAATTGTG	49161
QY	8215	ACATAGACATATCTTGTGTAATTCATCTTGTGTTTCTTAATATACATAGTCAGATTA	8274	QY	9295	ATGACTGGCACCTGTAAATATCAGAGCTTGTGCTGATTTGCTCTCATTTGACGGCAACA	9354
Db	48082	ACATAGACATATCTTGTGTAATTCATCTTGTGTTTCTTAATATACATAGTCAGATTA	48141	Db	49162	ATGACTGGCACCTGTAAATATCAGAGCTTGTGCTGATTTGCTCTCATTTGACGGCAACA	49221
QY	8275	TATATATTACTTTATGTTCTTAGATCCCGTGTAGCCCTTATTTTGTGATTTGTCCCAT	8334	QY	9355	AAAGTGTGCTTTGGGATAAGCAAGCCCTGGGCACTTTTCTAAGTGTCTTCTGA	9414
Db	48142	TATATATTACTTTATGTTCTTAGATCCCGTGTAGCCCTTATTTTGTGATTTGTCCCAT	48201	Db	49222	AAAGTGTGCTTTGGGATAAGCAAGCCCTGGGCACTTTTCTAAGTGTCTTCTGA	49281
QY	8335	TTTCCTTTTAGATTCTAAACTTGGTCATGGCACCATTAAACAATTCATAGCATTTTACA	8394	QY	9415	TTGTTTCAGGATTTTCTGCTGCTTTATATTAAGCAACCTGAGCAGGATATATGCTGT	9474
Db	48202	TTTCCTTTTAGATTCTAAACTTGGTCATGGCACCATTAAACAATTCATAGCATTTTACA	48261	Db	49282	TTGTTTCAGGATTTTCTGCTGCTTTATATTAAGCAACCTGAGCAGGATATATGCTGT	49341
QY	8395	GTTTTTGAATAATTTGCACAGGCATATTTTCTTTTCTTTTACCCCTCAGACAAATCT	8454	QY	9475	TTGCTGATAAGAAAGAGAAAATGAATTTGGCAGACACCTTTTCCAGACAGAGAGAG	9534
Db	48262	GTTTTTGAATAATTTGCACAGGCATATTTTCTTTTCTTTTACCCCTCAGACAAATCT	48321	Db	49342	TTGCTGATAAGAAAGAGAAAATGAATTTGGCAGACACCTTTTCCAGACAGAGAGAG	49401
QY	8455	TTACATGTTGAAAGGATCATATATGCTCCCTTATATAGTGTGATGATGATGATGATG	8514	QY	9535	CACATATTGAACAAAGTGGAAATTTGGACTGCTTACTGGATGATCACACACTGATGTC	9594
Db	48322	TTACATGTTGAAAGGATCATATATGCTCCCTTATATAGTGTGATGATGATGATGATG	48381	Db	49402	CACATATTGAACAAAGTGGAAATTTGGACTGCTTACTGGATGATCACACACTGATGTC	49461
QY	8515	AGTACCTCTCCAGGGTCTTCCCTGACTTGGACCTGGACAGGACCTGGGATCAGGAC	8574	QY	9595	AAAGCTTTCAGATCATGTAATAGTCTTAGTTTCAGTACACAGACTTGAAGAAAGGAAGA	9654
Db	48382	AGTACCTCTCCAGGGTCTTCCCTGACTTGGACCTGGACAGGACCTGGGATCAGGAC	48441	Db	49462	AAAGCTTTCAGATCATGTAATAGTCTTAGTTTCAGTACACAGACTTGAAGAAAGGAAGA	49521
QY	8575	ATTTAAGCTCTAGCATATTTGACTTGAAGGCTCTCTAATCATGCTTCAATTTCTTTT	8634	QY	9655	AAGCAAGGCTGATTTGAGGGCATGTAGAAAATGAAAAGCCCTTATCTGAGAAAACAAAC	9714
Db	48442	ATTTAAGCTCTAGCATATTTGACTTGAAGGCTCTCTAATCATGCTTCAATTTCTTTT	48501	Db	49522	AAGCAAGGCTGATTTGAGGGCATGTAGAAAATGAAAAGCCCTTATCTGAGAAAACAAAC	49581
QY	8635	ATGCTCAAGGTTGTCTGGCTCCCTCATGTAAGCCGAGGAGACCTGTGATGCTTTG	8694	QY	9715	TGGCGGTTATAGGTTATCTGGTCACCTTTAAAGGGAAGGAACACTGAATTAATATAGA	9774
Db	48502	ATGCTCAAGGTTGTCTGGCTCCCTCATGTAAGCCGAGGAGACCTGTGATGCTTTG	48561	Db	49582	TGGCGGTTATAGGTTATCTGGTCACCTTTAAAGGGAAGGAACACTGAATTAATATAGA	49641
QY	8695	CTTGAACCTTTCTCTAGTGAAGTTAGATGCTTGGAGTCCCTTGCACACTCATGCATCAC	8754	QY	9775	GCTGAAGGCACTTCTGTAATAGGTACCTTCACACAACTTTCTTATTTCTTGAGCTATG	9834
				Db	49642	GCTGAAGGCACTTCTGTAATAGGTACCTTCACACAACTTTCTTATTTCTTGAGCTATG	49701



QY	9835	ATTACAGCTGGAGCACACAAACAGAAATAAATAATCCACTGGCGGCAACAGCATTT	9894	10913	AGTCCCAAGACACAGACTACTCAGTTAAAAAGACATAAATGACAAACAGCTCAACAGTGTTA	10972
Db	49702	ATTACAGCTGGAGCACACACACAGAAATAAATAATCCACTGGCGGCAACAGCATTT	49761	50782	AGTCCCAAGACACAGACTACTCAGTTAAAAAGACATAAATGACAAACAGCTCAACAGTGTTA	50841
QY	9895	CTTAACACCTATGGTGCAAAATGGGATCTTGACTCTCTCCACTCTGGAACACACACA	9954	10973	TATTAAGAAGTTAAGCTTGAAGGTGACAAAAGCTGGGTATATAGTGGGAGTTTATACAT	11032
Db	49762	CTTAACACCTATGGTGCAAAATGGGATCTTGACTCTCTCCACTCTGGAACACACACA	49821	50842	TATTAAGAAGTTAAGCTTGAAGGTGACAAAAGCTGGGTATATAGTGGGAGTTTATACAT	50901
QY	9955	AAGCAGGGAACCTGACGCTACTTAATGAGGTGACATGACCAATCTGGTGGTTCA	10014	11033	GCTCATCAATTTTGAATGCAATCATGATATCTGTCATATTTACTTCAAAATAGATGCG	11092
Db	49822	AAGCAGGGAACCTGACGCTACTTAATGAGGTGACATGACCAATCTGGTGGTTCA	49881	50902	GCTCATCAATTTTGAATGCAATCATGATATCTGTCATATTTACTTCAAAATAGATGCG	50961
QY	10015	TACCACCATCAAAATCAAAAGATGCTCAGTTTTCGAAATPACCTCATCAAAAAGATATT	10074	11093	TTCTGTGAGACTCTAGGGTTACTATGAGGTGTACTCAGTTGCGAGTTTAACTTTACAGAA	11152
Db	49882	TACCACCATCAAAATCAAAAGATGCTCAGTTTTCGAAATPACCTCATCAAAAAGATATT	49941	50962	TTCTGTGAGACTCTAGGGTTACTATGAGGTGTACTCAGTTGCGAGTTTAACTTTACAGAA	51021
QY	10075	TAACTACAGTTACTCAGCTTGTGGCAATAAAGCTCTGGAATAATCTTACCATAAAGCT	10134	11153	CTAAATAGTTAAATGATTTTGACAGCACTTACAGGATTAATGACATACATGTTTCAGGCTA	11212
Db	49942	TAACTACAGTTACTCAGCTTGTGGCAATAAAGCTCTGGAATAATCTTACCATAAAGCT	50001	51022	CTAAATAGTTAAATGATTTTGACAGCACTTACAGGATTAATGACATACATGTTTCAGGCTA	51081
QY	10135	ATTACACTAATAAACAATACAGGCAGAAAAGCTATCTGCTGAGTCTGTTCTGTTT	10194	11213	CCAATTCACAAAACATAATGGAAGCTTGGGAGGCTGATGTAAGCTAGATTGAGAGGCTA	11272
Db	50002	ATTACACTAATAAACAATACAGGCAGAAAAGCTATCTGCTGAGTCTGTTCTGTTT	50061	51082	CCAATTCACAAAACATAATGGAAGCTTGGGAGGCTGATGTAAGCTAGATTGAGAGGCTA	51141
QY	10195	ATTGAGAAATAAATAAGGCTGTTAAGG-CTTGTAAACAGTTCTCAAATTAATGGCTGAC	10253	11273	AGCATTTGGGTATCAGTATGACACAGATGGGCTTGTCTGCTTGGGAGTAGCTTGGCCCC	11332
Db	50062	ATTGAGAAATAAATAAGGCTGTTAAGGCTTGTAAAGCTTGTAAACAGTTCTCAAATTAATGGCTGAC	50121	51142	AGCATTTGGGTATCAGTATGACACAGATGGGCTTGTCTGCTTGGGAGTAGCTTGGCCCC	51201
QY	10254	TTAGGAACACAGTACGTTATTCAGGACAAATGATTAATAACCCAAATCATTAAGAG	10313	11333	ATGTGGCAAGTTTGGCGCTTTGGCAGGAAGGCTGATGTAAGCTAGATTGAGAGGCTA	11392
Db	50122	TTAGGAACACAGTACGTTATTCAGGACAAATGATTAATAACCCAAATCATTAAGAG	50181	51202	ATGTGGCAAGTTTGGCGCTTTGGCAGGAAGGCTGATGTAAGCTAGATTGAGAGGCTA	51261
QY	10314	TTTAAGATCTCTCTTTTTTTTTTTTTTTTTTTTTTTTGAGATGGAGTTTCAGTCTCTTG	10373	11393	AAGGTGTGCAGTTTGTAAATCTTAAACAAGGAGTTCCTAACTTGTAAAGTGAGTCATCAG	11452
Db	50182	TTTAAGATCTCTCTCTTTTTTTTTTTTTTTTTTTTTTTTGAGATGGAGTTTCAGTCTCTTG	50241	51262	AAGGTGTGCAGTTTGTAAATCTTAAACAAGGAGTTCCTAACTTGTAAAGTGAGTCATCAG	51321
QY	10374	CCCAGGCTAGAGTGCAATGGTGTGATCCCGGGTCACTGCAACCTCCACCTCCCGGGTTCA	10433	11453	GAAGAAATGTAATCAGAACTGAGAACCCAGCAGCCAGGCTCTCATCTAAATTCACACCACA	11512
Db	50242	CCCAGGCTAGAGTGCAATGGTGTGATCCCGGGTCACTGCAACCTCCACCTCCCGGGTTCA	50301	51322	GAAGAAATGTAATCAGAACTGAGAACCCAGCAGCCAGGCTCTCATCTAAATTCACACCACA	51381
QY	10434	AGTGATCTCGCTCAGCTCCCAAGTAGCTGGGACTACAGCAGGTGCGACAGGCC	10493	11513	TCGTCTGTACITTTATAGTCTTCAGATGCTTCATTCACCCAGTATCCCGAGTGTGATA	11572
Db	50302	AGTGATCTCGCTCAGCTCCCAAGTAGCTGGGACTACAGCAGGTGCGACAGGCC	50361	51382	TCGTCTGTACITTTATAGTCTTCAGATGCTTCATTCACCCAGTATCCCGAGTGTGATA	51441
QY	10494	TGGCTAATTTTGTATTTTAGTAGAGAT-GGGTTTCCCCAGCTGGCCAGGCTGGTCTT	10552	11573	GAAGCACATGTTTATCATTTGCCATGTCGAAGTAGAGTAACTAACTTTTATTAAGCAG	11632
Db	50362	TGGCTAATTTTGTATTTTAGTAGAGATGGGTTTCCCCAGCTGGCCAGGCTGGTCTT	50421	51442	GAAGCACATGTTTATCATTTGCCATGTCGAAGTAGAGTAACTAACTTTTATTAAGCAG	51501
QY	10553	GAACCTCTGACCTCAGGTGATCTGCCTGCCTCAGCCTCCCAAAATGCTGGGATTACAGGC	10612	11633	TCATATAACATTTACTGTTCTGGATCATATCTTTATTTCTTTTGTGCAATTTACCTAGCATTT	11692
Db	50422	GAACCTCTGACCTCAGGTGATCTGCCTGCCTCAGCCTCCCAAAATGCTGGGATTACAGGC	50481	51502	TCATATAACATTTACTGTTCTGGATCATATCTTTATTTCTTTTGTGCAATTTACCTAGCATTT	51561
QY	10613	ATGAGGACATGGCGCCGGTCTCTTCCCTAACTTCAACACAGGCTGTTTTCAGCACACACA	10672	11693	CAACCACCAATTTGTTTTTATTTCTTACACAAATTTTAAAGATTTTGGGGGAGGATAA	11752
Db	50482	ATGAGGACATGGCGCCGGTCTCTTCCCTAACTTCAACACAGGCTGTTTTCAGCACACACA	50541	51562	CAACCACCAATTTGTTTTTATTTCTTACACAAATTTTAAAGATTTTGGGGGAGGATAA	51621
QY	10673	GTTTCTCAGGAAAAAAGCTCTCTTTTGATCTCTTTCATGCTTATAGCTTTATA	10732	11753	AGTGTAAACAACAGATATGAATGATGTAATTTTCAGGTTTTCCTGGGAACTCAAAATTTG	11812
Db	50542	GTTTCTCAGGAAAAAAGCTCTCTTTTGATCTCTTTCATGCTTATAGCTTTATA	50601	51622	AGTGTAAACAACAGATATGAATGATGTAATTTTCAGGTTTTCCTGGGAACTCAAAATTTG	51681
QY	10733	AAAAATGTACACAGAGTCAATATTTTAAAGGATGCTAGTGAATTTCTGAACCTTAAG	10792	11813	TAGTGTATTTAGGGATTAAGTGAAGAACCTGAGGCCCTGGGAGTTTAAAGTGGCTGG	11872
Db	50602	AAAAATGTACACAGAGTCAATATTTTAAAGGATGCTAGTGAATTTCTGAACCTTAAG	50661	51682	TAGTGTATTTAGGGATTAAGTGAAGAACCTGAGGCCCTGGGAGTTTAAAGTGGCTGG	51741
QY	10793	TGACTACAGCAAAATATCTTGAGAAAGGATACATATTTTCTCCCTCGAGTAATTA	10852	11873	TCCTCAGTTCCCTCCATGTCGCAAGAGTGGAAACAGACCCACATCTTTTCTAGTCTCT	11932
Db	50662	TGACTACAGCAAAATATCTTGAGAAAGGATACATATTTTCTCCCTCGAGTAATTA	50721	51742	TCCTCAGTTCCCTCCATGTCGCAAGAGTGGAAACAGACCCACATCTTTTCTAGTCTCT	51801
QY	10853	CTCAACCTGAGCAATAATCAGACAGTGGCTGGCATTTGTAACAGAGGACTGATATCA	10912	11933	GCAAGTTTCTGCTCTATTTGCCCTCTCTTGGTAGAAAAACATCACACACCATGAGGCTTC	11992
Db	50722	CTCAACCTGAGGCAATAATCAGACAGTGGCTGGCATTTGTAACAGAGGACTGATATCA	50781	51802	GCAAGTTTCTGCTCTATTTGCCCTCTCTTGGTAGAAAAACATCACACACCATGAGGCTTC	51861
				11993	ACTTAAAGGTGGAGAAAGGACAGAGGACAGAGACTCCACAAAGTTCTAGCTATGAGGTT	12052

51862	ACTTAAAGGTGGAGAAAGGACAGAGCGAGAGACTCCAAAGTTCTAGCTATGAGTT	51921		Db
12053	TCCAAAAAATAACAGAAAAAGAGATTCTTCTGACCTTTATTTATGTTAGGTATGAATCATG	12112		QY
51922	TCCAAAAAATAACAGAAAAAGAGATTCTTCTGACCTTTATTTATGTTAGGTATGAATCATG	51981		Db
12113	ACCCAAAACTCCCTCCCTATTTGCTAGAGAGGAAAACTCCTTGGCGGAAATTTATTTTC	12172		QY
51982	ACCCAAAACTCCCTCCCTATTTGCTAGAGAGGAAAACTCCTTGGCGGAAATTTATTTTC	52041		Db
12173	TGTTCTTTGGTCTCAATTTGAAATTTAGTACTTTTTTTTCAATAACAGAGCTTTCAA	12232		QY
52042	TGTTCTTTGGTCTCAATTTGAAATTTAGTACTTTTTTTTCAATAACAGAGCTTTCAA	52101		Db
12233	ACATGTAAAAACAAAGTACTATTCTTTTACCTCAAACTCAAGGTCAACAGTGTATTACT	12292		QY
52102	ACATGTAAAAACAAAGTACTATTCTTTTACCTCAAACTCAAGGTCAACAGTGTATTACT	52161		Db
12293	CTAACCTCATATTTTCATGTAATAACAGATGCTCGTTGACTTATGATGGGCTATATCC	12352		QY
52162	CTAACCTCATATTTTCATGTAATAACAGATGCTCGTTGACTTATGATGGGCTATATCC	52221		Db
12353	TGATAAACCCATTGGAGGTTAAAAATATTTTAAAGTTGAAAAATCATTAACCCCCCAT	12412		QY
52222	TGATAAACCCATTGGAGGTTAAAAATATTTTAAAGTTGAAAAATCATTAACCCCCCAT	52281		Db
12413	AAACCCACTGAAAGTAAAAAATAAATCTAAATCTAACTCATTTGAGGATTAATCT	12472		QY
52282	AAACCCACTGAAAGTAAAAAATAAATCTAAATCTAACTCATTTGAGGATTAATCT	52341		Db
12473	GTACCAATTTATTAATACATCTCTAACTCTTAACTGTGATAAAATGCAATGTTTAAAT	12532		QY
52342	GTACCAATTTATTAATACATCTCTAACTCTTAACTGTGATAAAATGCAATGTTTAAAT	52401		Db
12533	ACAAAATCTACCTTAGAACAGAGAAGTCATTTTTTTTCAATTTTGTCTAGATGCTA	12592		QY
52402	ACAAAATCTACCTTAGAACAGAGAAGTCATTTTTTTTCAATTTTGTCTAGATGCTA	52461		Db
12593	AGTGATTTCTAGATGCTATAAATGTGCCAGAAATCAGAGATAGGTATAGGCTTGCCATTC	12652		QY
52462	AGTGATTTCTAGATGCTATAAATGTGCCAGAAATCAGAGATAGGTATAGGCTTGCCATTC	52521		Db
12553	AACAAGTAGTCAGGCGCTTGTGGTAAATTTAAATTTCAATTTAGTTTAAACATAAAA	12712		QY
52522	AACAAGTAGTCAGGCGCTTGTGGTAAATTTAAATTTCAATTTAGTTTAAACATAAAA	52581		Db
12713	ATTAAAAATTTAGTTTCTATTTTGTCTACACACATTTCAAGTGCCCAACAGCCACATGT	12772		QY
52582	ATTAAAAATTTAGTTTCTATTTTGTCTACACACATTTCAAGTGCCCAACAGCCACATGT	52641		Db
12773	GCTAGTGACTACCATATGGAACATTCGAAATATAGGTTATTCCTATCACTACAGGAAGAT	12832		QY
52642	GCTAGTGACTACCATATGGAACATTCGAAATATAGGTTATTCCTATCACTACAGGAAGAT	52701		Db
12833	CTATTAGACAGTGCAGGTGTTAGTCAAGCATCTTGAGAAAATATATGAGAGGAACA	12892		QY
52702	CTATTAGACAGTGCAGGTGTTAGTCAAGCATCTTGAGAAAATATATGAGAGGAACA	52761		Db
12893	GAGGAAATTAACATCTATCTTTATCTCTTGTAGCTTCTCTATGTTTGGCTGTGACTA	12952		QY
52762	GAGGAAATTAACATCTATCTTTATCTCTTGTAGCTTCTCTATGTTTGGCTGTGACTA	52821		Db
12953	AATGGATPACAGCCAGGCGACCAATCATGAAAAACAGTTGAGTAAATTTAATAGGTCA	13012		QY
52822	AATGGATPACAGCCAGGCGACCAATCATGAAAAACAGTTGAGTAAATTTAATAGGTCA	52881		Db
13013	CTATACTTTGGAAATATCTCTCTCTCATTTATACACTATCAAGAGAGAGACTGAA	13072		QY
52882	CTATACTTTGGAAATATCTCTCTCTCATTTATACACTATCAAGAGAGAGACTGAA	52941		Db
13073	ATAATAGTTTCTTAAATTTGTCTACACAATACGTTTTTCTGGAATCCCTCTTTTAAACAA	13132		QY

Qy	14213	TAGAAGCTTTCCAGTTTCCAGATTTAAATTCCTTAAGGTTTGAGCACTGAAATATTGTG	14272	Qy	15293	ACATTTTTTTTCCCTTTGAAACAGTGGGTGGATCAAGCAATCTTATGACTTAAGAAAA	15352
Db	54082	TAGAAGCTTTCCAGTTTCCAGATTTAAATTCCTTAAGGTTTGAGCACTGAAATATTGTG	54141	Db	55162	ACATTTTTTTTCCCTTTGAAACAGTGGGTGGATCAAGCAATCTTATGACTTAAGAAAA	55221
Qy	14273	GAGAAACACAGAGCCGTGTTATGTGACAGGTCTCAATACCCCTTAAAGGTTGCTCATCT	14332	Qy	15353	TATGTTCCATGTAGGCTAAATAGTGTTCCTCTGCTGCTGAAGTAAGTATGGTCAATGGTG	15412
Db	54142	GAGAAACACAGAGCCGTGTTATGTGACAGGTCTCAATACCCCTTAAAGGTTGCTCATCT	54201	Db	55222	TATGTTCCATGTAGGCTAAATAGTGTTCCTCTGCTGCTGAAGTAAGTATGGTCAATGGTG	55281
Qy	14333	TTACAGAACTCATTTTCATCTCATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT	14392	Qy	15413	AACAAATTTCCATGATTTTCCAAAGTTGAAATATCAATATATACATCTCATCTTATGCTTA	15472
Db	54202	TTACAGAACTCATTTTCATCTCATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT	54261	Db	55282	AACAAATTTCCATGATTTTCCAAAGTTGAAATATCAATATATACATCTCATCTTATGCTTA	55341
Qy	14393	TCATTTCTCAGAGTAAGATACAGACACAGATTCAGAAATTAAGGACTAGAAATTTTCC	14452	Qy	15473	ATCCAGAAGTTACTCTCTAACTTACTACGATTTTGTGTTGTTTTCAGAAATAGAAATCAA	15532
Db	54262	TCATTTCTCAGAGTAAGATACAGACACAGATTCAGAAATTAAGGACTAGAAATTTTCC	54321	Db	55342	ATCCAGAAGTTACTCTCTAACTTACTACGATTTTGTGTTGTTTTCAGAAATAGAAATCAA	55401
Qy	14453	CTAATGAGCTAGCTCAAGAACCCCTCTCTGGAATGGAATAGCCCTTTTGTGTT	14512	Qy	15533	AACCAAAACACCCACCACCAAGCCCTCAAAAACAGTTTACAAAGCTGGAGAT	15592
Db	54322	CTAATGAGCTAGCTCAAGAACCCCTCTCTGGAATGGAATAGCCCTTTTGTGTT	54381	Db	55402	AACCAAAACACCCACCACCAAGCCCTCAAAAACAGTTTACAAAGCTGGAGAT	55461
Qy	14513	TCCACAGGCACTTGACAGTGAATTTGACACATCTCAAGGATTTTCAAGGACTC	14572	Qy	15593	TTTGTGTTAGAGAGAACTTACCTTATTCCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	15652
Db	54382	TCCACAGGCACTTGACAGTGAATTTGACACATCTCAAGGATTTTCAAGGACTC	54441	Db	55462	TTTGTGTTAGAGAGAACTTACCTTATTCCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	55521
Qy	14573	AGGGCATATGACAGGAGTGTGTTCCAGGTAAGCAGTTTACTGGCTGGTGGATGTT	14632	Qy	15653	TATACTTTAAGTTGTGGGATCTGTGTCAGAACGTCAGAGTTGTTTACGTAGGTATACAC	15712
Db	54442	AGGGCATATGACAGGAGTGTGTTCCAGGTAAGCAGTTTACTGGCTGGTGGATGTT	54501	Db	55522	TATACTTTAAGTTGTGGGATCTGTGTCAGAACGTCAGAGTTGTTTACGTAGGTATACAC	55581
Qy	14633	TATTTTCCCTTTCATCCAGCACTTGACAGAGTGATTTTATGAGCTTTGACAGTTCTAG	14692	Qy	15713	GTGCCATGGTGGTTGCTGTCACCCCTTTAACCCATCAGCTACATAGGTATTTCTCCCTAAT	15772
Db	54502	TATTTTCCCTTTCATCCAGCACTTGACAGAGTGATTTTATGAGCTTTGACAGTTCTAG	54561	Db	55582	GTGCCATGGTGGTTGCTGTCACCCCTTTAACCCATCAGCTACATAGGTATTTCTCCCTAAT	55641
Qy	14693	AAGTAAATATTAGGACACATGCTTAAAGAGATGCTTTAGATACAGTTTCAAGGATG	14752	Qy	15773	GCTATCCCTCCCAACCCCAACCCACCCAGCCAGCCAGTGTGATGTTCCCTTCCCTCC	15832
Db	54562	AAGTAAATATTAGGACACATGCTTAAAGAGATGCTTTAGATACAGTTTCAAGGATG	54621	Db	55642	GCTATCCCTCCCAACCCCAACCCACCCAGCCAGCCAGTGTGATGTTCCCTTCCCTCC	55701
Qy	14753	CCATGTTTCAAAATCCACTCATGCGACTGAACAAAGAGATCAAGAGTTTCCCTCTACA	14812	Qy	15833	TGTGTCCTCTGTTTCAACTCTCACTTATGAGTGAGAACATGCTGGTGGTGGTGGTGGTGGT	15892
Db	54622	CCATGTTTCAAAATCCACTCATGCGACTGAACAAAGAGATCAAGAGTTTCCCTCTACA	54681	Db	55702	TGTGTCCTCTGTTTCAACTCTCACTTATGAGTGAGAACATGCTGGTGGTGGTGGTGGTGGT	55761
Qy	14813	CATTAAGTGAACAGAGAAATTTGCAAGTAATGTTTATGTTAGAGAGATGAAGAAAGGAA	14872	Qy	15893	CTGTGTTAGTTGCTGAGAAATGATGTTTCTAGCTTCATCCGCTGCTCTGCAAGAGCG	15952
Db	54682	CATTAAGTGAACAGAGAAATTTGCAAGTAATGTTTATGTTAGAGAGATGAAGAAAGGAA	54741	Db	55762	CTGTGTTAGTTGCTGAGAAATGATGTTTCTAGCTTCATCCGCTGCTCTGCAAGAGCG	55821
Qy	14873	CTAAGAGAGAGGTTAGCAGGCTTCAAGTGTCTTCAAACTAACTGGCTGGGAGCA	14932	Qy	15953	TGAATCATCTCTTTTAAAGCTGCAAGATTTCCATGTTGTTATGTTGTTGTTGTTGTTGTTGTT	16012
Db	54742	CTAAGAGAGAGGTTAGCAGGCTTCAAGTGTCTTCAAACTAACTGGCTGGGAGCA	54801	Db	55822	TGAATCATCTCTTTTAAAGCTGCAAGATTTCCATGTTGTTATGTTGTTGTTGTTGTTGTTGTT	16072
Qy	14933	AGGTCTTTGGGGTCTATGTTTCACTCTGCTCTTCCCACTAAAGTAATTTTAAATC	14992	Qy	15953	TGAATCATCTCTTTTAAAGCTGCAAGATTTCCATGTTGTTATGTTGTTGTTGTTGTTGTTGTT	16072
Db	54802	AGGTCTTTGGGGTCTATGTTTCACTCTGCTCTTCCCACTAAAGTAATTTTAAATC	54861	Db	55822	TGAATCATCTCTTTTAAAGCTGCAAGATTTCCATGTTGTTATGTTGTTGTTGTTGTTGTTGTT	16072
Qy	14993	AGCTAAATTTCTATCTGAGCATAGAGTCAAGATAAAATTAAGCACTCCCAAAATACA	15052	Qy	16013	TTATCCAGTCTATCACTGATGGGCAATTTGGGTTGGTTTCCAAAGTCTTTGCTATGTAATA	16072
Db	54862	AGCTAAATTTCTATCTGAGCATAGAGTCAAGATAAAATTAAGCACTCCCAAAATACA	54921	Db	55882	TTATCCAGTCTATCACTGATGGGCAATTTGGGTTGGTTTCCAAAGTCTTTGCTATGTAATA	16072
Qy	15053	TCAAAGTCTGACCTTCAATGTTCTTCTCAGAGTTTACTACTAGGTAGAGACCTTGTAC	15112	Qy	16073	GTGCTGCAATTAACATATGTTGCTATGTTCTTTATAGCAGATGATCTATATCATTTT	16131
Db	54922	TCAAAGTCTGACCTTCAATGTTCTTCTCAGAGTTTACTACTAGGTAGAGACCTTGTAC	54981	Db	55942	GTGCTGCAATTAACATATGTTGCTATGTTCTTTATAGCAGATGATCTATATCATTTT	16131
Qy	15113	TTCTAGATTTTAACTATAACCTGATTCTGCTATCTGCAATTTTCTTGGGGTATG	15172	Qy	16073	GTGCTGCAATTAACATATGTTGCTATGTTCTTTATAGCAGATGATCTATATCATTTT	16131
Db	54982	TTCTAGATTTTAACTATAACCTGATTCTGCTATCTGCAATTTTCTTGGGGTATG	55041	Db	55942	GTGCTGCAATTAACATATGTTGCTATGTTCTTTATAGCAGATGATCTATATCATTTT	16131
Qy	15173	ATTAAGGTTTAAATTTAGGTTCTTAGAGTGAAGGACAACTCAATCTAGAGTTCA	15232	Qy	16132	GGTATATACCCAGTAATGGGATGCTGCTGGACACTGATGGAGCACTCAAAACAGTAAT	16191
Db	55042	ATTAAGGTTTAAATTTAGGTTCTTAGAGTGAAGGACAACTCAATCTAGAGTTCA	55101	Db	56002	GGTATATACCCAGTAATGGGATGCTGCTGGACACTGATGGAGCACTCAAAACAGTAAT	16191
Qy	15233	TCAGTTTCAATCAAAATTAACCAATGAACATAGATGATGATCTCTAGATATGAGA	15292	Qy	16192	TCCTAAACATGATGTTGCTTCAATTTATTTATTTTAAACATATTTTTCGCAATGA	16251
Db	55102	TCAGTTTCAATCAAAATTAACCAATGAACATAGATGATGATCTCTAGATATGAGA	55161	Db	56062	TCCTAAACATGATGTTGCTTCAATTTATTTATTTTAAACATATTTTTCGCAATGA	16251

56242	GTCAAAACTTTAGTACCTTGCATGTGTTCCACAATAAAGTAATTAGAGCTGCTGCC	56301		Db
16432	TATGTCACGGAAGAGCTTAACCTCCTCTTCAGTCTACTCTCTCTCTCTCTCTATGTGT	16491		Qy
56302	TATGTCACGGAAGAGCTTAACCTCCTTCAGTCTACTCTCTCTCTCTCTCTATGTGT	56361		Db
16492	GTGTGTCGTGTATATATATATATATATATATACACACACACACACACATATATAT	16551		Qy
56362	GTGTGTCGTGTATATATATATATATATATATACACACACACACATATATATAT	56419		Db
16552	ATATATATATGTAATTTTTTTTTTTTGAGATGGAGTTCCTTTACCCAGGCTGGAGTGCAAT	16611		Qy
56420	ATATATATATGTAATTTTTTTTTTTTGAGATGGAGTTCCTTTTACCCAGGCTGGAGTGCAAT	56479		Db
16612	GGCCGATCTCAGCTCAGCTGCAACCTCCGCTCCGCTCCGCTTCAAGTGATTTCCCGCCTCA	16671		Qy
56480	GGCCGATCTCAGCTCAGCTGCAACCTCCGCTCCGCTCCGCTTCAAGTGATTTCCCGCCTCA	56539		Db
16672	GCTTCCTGAGTACGTGGGATTTACAGTGGCTGCCATCAGCCCTGGCTTAATTTTTGTATTT	16731		Qy
56540	GCCTCTGAGTACGTGGGATTTACAGTGGCTGCCATCAGCCCTGGCTTAATTTTTGTATTT	56599		Db
16732	TTAGTAGAGAGGGGTTTTGCCATGTGGCCACGCTGTTCTTTGAATCCTCGACCTCAGGT	16791		Qy
56600	TTAGTAGAGAGGGGTTTTGCCATGTGGCCACGCTGTTCTTTGAATCCTCGACCTCAGGT	56659		Db
16792	GATCCACCCACCTCGCCCTCCCAAGCTGCTAGATTTACAGGCGGTGAGCCACTGCGCCCGG	16851		Qy
56660	GATCCACCCACCTCGCCCTCCCAAGCTGCTAGATTTACAGGCGGTGAGCCACTGCGCCCGG	56719		Db
16852	CCTATCTTTTATGCTCAATAAAGTGTATATATTTACTAGTGATAAGAAAAACATAGACC	16911		Qy
56720	CCTATCTTTTATGCTCAATAAAGTGTATATATTTACTAGTGATAAGAAAAACATAGACC	56779		Db
16912	CTGGAACCACTGATGGAGTTGGAGTCTGGCTGCTGCTGATTTACTGACGAGCCATGCT	16971		Qy
56780	CTGGAACCACTGATGGAGTTGGAGTCTGGCTGCTGCTGATTTACTGACGAGCCATGCT	56839		Db
16972	GGCCAACTTACTGATCCTCTTAGGGCTCAGTTTACTCAGCTATAAAAAAGAAATAAAAT	17031		Qy
56840	GGCCAACTTACTGATCCTCTTAGGGCTCAGTTTACTCAGCTATAAAAAAGAAATAAAAT	56899		Db
17032	AGTGACATTTTACAATATTTGATGGGTGCTTAATGAGCTAAATGATGATTTACTTCAATA	17091		Qy
56900	AGTGACATTTTACAATATTTGATGGGTGCTTAATGAGCTAAATGATGATTTACTTCAATA	56959		Db
17092	GTTTTGTCAAGCAATAAATGCCATTTGTACTATATTAAGGTTATTGTGCTTTTAAGT	17151		Qy
56960	GTTTTGTCAAGCAATAAATGCCATTTGTACTATATTAAGGTTATTGTGCTTTTAAGT	57019		Db
17152	TTTTTGTCCCTCATATCTTTTACCTTTTGTCTATTTTGCATAATPCCAAAGAGCTGATTC	17211		Qy
57020	TTTTTGTCCCTCATATCTTTTACCTTTTGTCTATTTTGTCTATTTTGC	57079		Db
17212	CCTGAGTAGCATTAAATAGTTAAATAAAGTGGAGTTCCTGGTTGAACATACCTTC	17271		Qy
57080	CCTGAGTAGCATTAAATAGTTAAATAAAGTGGAGTTCCTGGTTGAACATACCTTC	57139		Db
17272	ATATTTAGAAAAATAAAGATCTTTGACAAATTTATATTTTGTCTATCTTTATTTGCCAAA	17331		Qy
57140	ATATTTAGAAAAATAAAGATCTTTGACAAATTTATATTTTGTCTATCTTTATTTGCCAAA	57199		Db
17332	TTTTTAAATGATATAATTTGAATTAAGTTTGTCTATGAGATTTGGCGTCATATCTTG	17391		Qy
57200	TTTTTAAATGATATAATTTGAATTAAGTTTGTCTATGAGATTTGGCGTCATATCTTG	57259		Db
17392	TAAATGAATAACATCATATTTCTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	17451		Qy
57260	TAAATGAATAACATCATATTTCTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	57319		Db
17452	AAATTTACTGATCACATATTTGATTTATATATTTCTTAACATATTTGATTTGATPCCATGG	17511		Qy
57377	AAATTTACTGATCACATATTTGATTTATATATTTCTAAACAATGTTGATGTTCCACATGG	57377		Db
17512	TGTATTTGTTCAAAATTTAGAAAAACAGTGCCTTCGTCCAGGATPAGGATTAACCTGTCATCAG	17571		Qy
57380	TGTATTTGTTCAAAATTTAGAAAAACAGTGCCTTCGTCCAGGATPAGGATTAACCTGTCATCAG	57439		Db
17572	GACACTTTGGCTTGGCAACCTTAGTGTGGGTAGAATTTCTGCTCCTTAATCAAAACCTCGCT	17631		Qy
57440	GACACTTTGGCTTGGCAACCTTAGTGTGGGTAGAATTTCTGCTCCTTAATCAAAACCTCGCT	57499		Db
17632	GGGTGCCCTTTGTGCAGTGAACAACCTGAACAACCTGTATGCAATGGCCCTGTCCTCTGAA	17691		Qy
57500	GGGTGCCCTTTGTGCAGTGAACAACCTGAACAACCTGTATGCAATGGCCCTGTCCTCTGAA	57559		Db
17692	TCCTATAGATTAAAGATTGCAACAAGAAATCTAAGAATGACATACCTCATGATACATTTTT	17751		Qy
57560	TCCTATAGATTAAAGATTGCAACAAGAAATCTAAGAATGACATACCTCATGATACATTTTT	57619		Db
17752	CACGGTTTTCCCTCAAAATTTGCATGTGCAGGACCTCCAGTGTGCAGTTCACAGCCACAAAT	17811		Qy
57620	CACGGTTTTCCCTCAAAATTTGCATGTGCAGGACCTCCAGTGTGCAGTTCACAGCCACAAAT	57679		Db
17812	TCCCTCCACAGCGCTGCACGAGGAGGCAACGCTGGAAGAAGACACACATTTGCCCCAATTCAG	17871		Qy
57680	TCCCTCCACAGCGCTGCACGAGGAGGCAACGCTGGAAGAAGACACACATTTGCCCCAATTCAG	57739		Db
17872	CTCTCTCTCTATATTTGACCGAGTAAATTTCTTGGGAGTGCACACTGTAGCGTTGCGCATCATC	17931		Qy
57740	CTCTCTCTCTATATTTGACCGAGTAAATTTCTTGGGAGTGCACACTGTAGCGTTGCGCATCATC	57799		Db
17932	ATTGAGCCTATCCAGGTCACACTGTAAACAAATACATGCATCTGTGAAGCAAAACACACAG	17991		Qy
57800	ATTGAGCCTATCCAGGTCACACTGTAAACAAATACATGCATCTGTGAAGCAAAACACACAG	57859		Db
17992	TAAACCAATTTGCTCAGCATGTGTTTTGGGAATAGAGTGGGAAGATCTGTGAGGACAA	18051		Qy
57860	TAAACCAATTTGCTCAGCATGTGTTTTGGGAATAGAGTGGGAAGATCTGTGAGGACAA	57919		Db
18052	CTTTAAATCCTGGGATTTAAATCCATCCTCAGGCTCTCAATTTACTGGGAACCTAAAGTAAAA	18111		Qy
57920	CTTTAAATCCTGGGATTTAAATCCATCCTCAGGCTCTCAATTTACTGGGAACCTAAAGTAAAA	57979		Db
18112	GACCTAATTTCTCTCTTGATCCCATCTACCTTTTGAAAAATAAACAACAAAAACAAACAA	18171		Qy
57980	GACCTAATTTCTCTCTTGATCCCATCTACCTTTTGAAAAATAAACAACAAAAACAAACAA	58039		Db
18172	ACAAAAACCTTGGCTAAAAATTCATGCTCTGGTTCAAAATTTCCCTTGCAATCTTTTTTATGCA	18231		Qy
58040	ACAAAAACCTTGGCTAAAAATTCATGCTCTGGTTCAAAATTTCCCTTGCAATCTTTTTTATGCA	58099		Db
18232	AAAAAAGTTCAGAGGAAGAAAAATGAAACATTTTGGCAAAATTAATAATTTGCCTTTATCT	18291		Qy
58100	AAAAAAGTTCAGAGGAAGAAAAATGAAACATTTTGGCAAAATTAATAATTTGCCTTTATCT	58159		Db
18292	TCAAAAAGACAAAAATAACTGCTTCTTCATTTCAATAATAATCTGACTCTAAGCCATCAC	18351		Qy
58160	TCAAAAAGACAAAAATAACTGCTTCTTCATTTCAATAATAATCTGACTCTAAGCCATCAC	58219		Db
18352	TTAAATATAATTTAAATTTATATCTTAGGACACATTTAGAGACAAACCTGTATTTATTTTAC	18411		Qy
58220	TTAAATATAATTTAAATTTATATCTTAGGACACATTTAGAGACAAACCTGTATTTATTTAC	58279		Db
18412	CTGCGAGTGAAATTTTCACACATAAATGCTAATAAAGAAAGGGTTTGTAGTTTATTTTAA	18471		Qy
58280	CTGCGAGTGAAATTTTCACACATAAATGCTAATAAAGAAAGGGTTTGTAGTTTATTTTAA	58339		Db
18472	CTTCAAAAGTTAAATCAACATGTTAGAGAAAAATGATTTTTTGTCTGTGGAATATGCTGCATA	18531		Qy
58340	CTTCAAAAGTTAAATCAACATGTTAGAGAAAAATGATTTTTTGTCTGTGGAATATGCTGCATA	58399		Db
18532	TTTGTGCACCTGGGTCCCTAGATGGCAGTATAGCATAGTGGTTAAGTCTTTGGAGCCGACAG	18591		Qy
58400	TTTGTGCACCTGGGTCCCTAGATGGCAGTATAGCATAGTGGTTAAGTCTTTGGAGCCGACAG	58459		Db

Qy	18592	TAAAGTTACAAC	TGCTTCAAT	CACATCATGCT	TATGTTCTCTTTAGTTGGAAGTTAT	186551	
Db	58460	TAAAGTTACAAC	TGCTTCAAT	CACATCATGCT	TATGTTCTCTTTAGTTGGAAGTTAT	58519	
Qy	18652	TTAATGGCTGCA	CTTCTGCTTCC	TATCATATACATG	TATCATTTTGAAGAAATTGAAT	18711	
Db	58520	TTAATGGCTGCA	CTTCTGCTTCC	TATCATATACATG	TATCATTTTGAAGAAATTGAAT	58579	
Qy	18712	GTAACTGGCT	-GC	ACTCAATGCCAGCT	ATTCTTACTAATCTTGATTCATCTGAATCTCC	18770	
Db	58580	GTAACTGGCT	GSC	ACTCAATGCCAGCT	ATTCTTACTAATCTTGATTCATCTGAATCTCC	58639	
Qy	18771	CCCTCTCACAT	CTCTTTCTTTT	AAAGTCAAA	TGGACAAAATTTAAAAATATACTACGTCT	18830	
Db	58640	CCCTCTCACAT	CTCTTTCTTTT	AAAGTCAAA	TGGACAAAATTTAAAAATATACTACGTCT	58699	
Qy	18831	TTCTCCCTCT	TTATGTTTCTT	CTTTGGACATAT	ATAAATGATTTATCAAGGATATGGT	18890	
Db	58700	TTCTCCCTCT	TTATGTTTCTT	CTTTGGACATAT	ATAAATGATTTATCAAGGATATGGT	58759	
Qy	18891	CAGTGGGACT	TTCTATGA	ACTAAAAGC	CACACAATATTTTCAAGCTAAAGTCATAAATATT	18950	
Db	58760	CAGTGGGACT	TTCTATGA	ACTAAAAGC	CACACAATATTTTCAAGCTAAAGTCATAAATATT	58819	
Qy	18951	TACTTTGAA	TTCAATTCG	CAATTTATGTG	TTACATAAATTAGATTTGATTTCTGTTCTCCA	19010	
Db	58820	TACTTTGAA	TTCAATTCG	CAATTTATGTG	TTACATAAATTAGATTTGATTTCTGTTCTCCA	58879	
Qy	19011	AGTCCATCCA	ATTATCC	ATCTTTGG	CGCCAAATCCTCTATTATGTGTCATACATACAT	19070	
Db	58880	AGTCCATCCA	ATTATCC	ATCTTTGG	CGCCAAATCCTCTATTATGTGTCATACATACAT	58939	
Qy	19071	GAGTATCT	TTCTCACA	AGAACACAG	TTTAGAACCAAGTCTCTTTGTCTGCACAGAACCCACC	19130	
Db	58940	GAGTATCT	TTCTCACA	AGAACACAG	TTTAGAACCAAGTCTCTTTGTCTGCACAGAACCCACC	58999	
Qy	19131	ACCTTTTCCA	ATG	CAGCCCTTGTG	CACAGGCCACACAGAAAGAAATCCCATGAAT	19190	
Db	59000	ACCTTTTCCA	ATG	CAGCCCTTGTG	CACAGGCCACACAGAAAGAAATCCCATGAAT	59059	
Qy	19191	GTTTAGG	CAGTTAT	CCACATGTT	CTATCTAACTCTAGCCCTGGTAAATGTTCTTAGGCTTA	19250	
Db	59060	GTTTAGG	CAGTTAT	CCACATGTT	CTATCTAACTCTAGCCCTGGTAAATGTTCTTAGGCTTA	59119	
Qy	19251	AACTGAA	CTGTTT	AGGAGAGG	AGAAAAAGCCCTTTGGGAGCAGAGTCAAAAGTC	19310	
Db	59120	AACTGAA	CTGTTT	AGGAGAGG	AGAAAAAGCCCTTTGGGAGCAGAGTCAAAAGTC	59179	
Qy	19311	AAGGACAG	TCTCAG	TAGATGAT	CTATAGGAAATTCGAGGAACAGTCTGGACCATGAG	19370	
Db	59180	AAGGACAG	TCTCAG	TAGATGAT	CTATAGGAAATTCGAGGAACAGTCTGGACCATGAG	59239	
Qy	19371	TCCACTA	AGCCGAT	CCCTGTTT	GTCTTTTTATCTACAACCTGTGCTTTGATTTCTCAAGG	19430	
Db	59240	TCCACTA	AGCCGAT	CCCTGTTT	GTCTTTTTATCTACAACCTGTGCTTTGATTTCTCAAGG	59299	
Qy	19431	GCAGG	GAATTTAT	CCCCAAAT	GTCTACACGTGAGCCCGAGATCTGTGGGAACTAAATAAA	19490	
Db	59300	GCAGG	GAATTTAT	CCCCAAAT	GTCTACACGTGAGCCCGAGATCTGTGGGAACTAAATAAA	59359	
Qy	19491	TGCAAA	TAACTACT	GTGCATAAT	TATTGCTGTGTTTTTTTCTTCCTTTGTAAGACATGT	19550	
Db	59360	TGCAAA	TAACTACT	GTGCATAAT	TATTGCTGTGTTTTTTTCTTCCTTTGTAAGACATGT	59419	
Qy	19551	CATAA	CTTTAG	CTATTAAT	CCAATCCAGATTTAAATTTGAATGAAC	TCTGTTCTTTGGGAAAGGA	19610
Db	59420	CATAA	CTTTAG	CTATTAAT	CCAATCCAGATTTAAATTTGAATGAAC	TCTGTTCTTTGGGAAAGGA	59479
Qy	19611	ACCA	TTTTAT	TGCTGCTA	AGCCCTGAAAAATAACTGCAAGC	AAAGGATTTACAT	19670
Db	59480	ACCA	TTTTAT	TGCTGCTA	AGCCCTGAAAAATAACTGCAAGC	AAAGGATTTACAT	59539

Qy	19671	AAATGGAA	TAAAGTGC	AGCAAA	TCAATCA	AGTGTCA	CACTTGA	GATAA	PACTGA	19733		
Db	59540	AAATGGAT	TAAAGTGC	AGCAATCA	TCAATCA	AGTGTCA	CACTTGA	GATAA	PACTGA	59599		
Qy	19731	TGCTGGCC	TGTGCAT	TCCTGG	CTGTGA	ACAGG	CGTGAT	GCAGAG	GCCAA	TCGCTG	19790	
Db	59600	TGCTGGCC	TGTGCAT	TCCTGG	CTGTGA	ACAGG	CGTGAT	GCAGAG	GCCAA	TCGCTG	59659	
Qy	19791	CTTGTG	ATAAT	GGAAAG	ATATTT	GTCTAA	CACGG	AGGACTAA	AGAGGT	ACAA	TTAGCAGG	19850
Db	59660	CTTGTG	ATAAT	GGAAAG	ATATTT	GTCTAA	CACGG	AGGACTAA	AGAGGT	ACAA	TTAGCAGG	59719
Qy	19851	AAGGGAT	CGTGAT	GTGTGA	AGAGG	CAGAGG	GACAGG	CAAGG	CGCAAC	AGCTG	AGTC	19910
Db	59720	AAGGGAT	CGTGAT	GTGTGA	AGAGG	CAGAGG	GACAGG	CAAGG	CGCAAC	AGCTG	AGTC	59779
Qy	19911	TCCTGCT	TTCCCT	CAGCC	CTCTG	CAACT	TATG	TCATA	ACCTT	TACAG	ATAGCTAC	19970
Db	59780	TCCTGCT	TTCCCT	CAGCC	CTCTG	CAACT	TATG	TCATA	ACCTT	TACAG	ATAGCTAC	59839
Qy	19971	AGTTGTT	TCC	CCAC	CCCAT	TTTCA	AGT	GAGT	ATATTT	TGCTAA	GAGTTAA	20030
Db	59840	AGTTGTT	TCC	CCAC	CCCAT	TTTCA	AGT	GAGT	ATATTT	TGCTAA	GAGTTAA	59899
Qy	20031	AACTGGA	ATTGA	AGCC	TTTCC	CCCTTT	TCTC	CAAT	AGTCT	CTGT	CAC	20090
Db	59900	AACTGGA	ATTGA	AGCC	TTTCC	CCCTTT	TCTC	CAAT	AGTCT	CTGT	CAC	59959
Qy	20091	GAGGGAT	GTCA	GTAA	GC	CAAT	TAGTT	GAAG	GAAG	AAG	CAAG	20150
Db	59960	GAGGGAT	GTCA	GTAA	GC	CAAT	TAGTT	GAAG	GAAG	AAG	CAAG	60019
Qy	20151	GGACTT	CTC	GTAT	GTGA	AC	AGG	TTGG	TGGT	GGTGA	T	20210
Db	60020	GGACTT	CTC	GTAT	GTGA	AC	AGG	TTGG	TGGT	GGTGA	T	60079
Qy	20211	AGAAG	CAC	CCCA	AGCC	AAAG	TAC	AG	CA	TGCCT	TCC	20270
Db	60080	AGAAG	CAC	CCCA	AGCC	AAAG	TAC	AG	CA	TGCCT	TCC	60139
Qy	20271	AGTGCC	CTC	CA	CAAA	CC	CAG	GAG	AG	CG	CA	20330
Db	60140	AGTGCC	CTC	CA	CAAA	CC	CAG	GAG	AG	CG	CA	60199
Qy	20331	TCAT	TGT	ATA	CT	CTTT	GAC	TAG	CA	TGTT	CT	20390
Db	60200	TCAT	TGT	ATA	CT	CTTT	GAC	TAG	CA	TGTT	CT	60259
Qy	20391	GATT	CA	AA	TTCT	GT	CAG	TTT	TAT	G	CA	20450
Db	60260	GATT	CA	AA	TTCT	GT	CAG	TTT	TAT	G	CA	60319
Qy	20451	AGTG	TG	ACT	GT	AG	AA	TCC	AC	CT	TC	20510
Db	60320	AGTG	TG	ACT	GT	AG	AA	TCC	AC	CT	TC	60379
Qy	20511	CTCA	ATT	TGA	AA	TTAG	AA	CTG	AA	AG	GT	20570
Db	60380	CTCA	ATT	TGA	AA	TTAG	AA	CTG	AA	AG	GT	60439
Qy	20571	GATT	GC	AG	ACT	TTT	CT	CAG	GG	AT	TTG	20630
Db	60440	GATT	GC	AG	ACT	TTT	CT	CAG	GG	AT	TTG	60499
Qy	20631	GCAG	CAG	AG	CGG	AC	CAG	AG	CG	CT	G	20690
Db	60500	GCAG	CAG	AG	CGG	AC	CAG	AG	CG	CT	G	60559
Qy	20691	TAGA	AG	GAG	AA	TTCT	AG	AG	TG	AG	ACT	20750
Db	60560	TAGA	AG	GAG	AA	TTCT	AG	AG	TG	AG	ACT	60619
Qy	20751	AGAG	AG	GAG	GG	CT	GG	CT	CT	CT	CT	20810

Db	60620		AGAGAGGGGCTGCCCTTCTGTTCCATCAGCTCCATAGCTGAACATTCAGAGCA	60679	Db	61700	AGCTGAATGGATTGATAGCAATGATTTGTCTCTCAGTGGGAACAAATGCGAGGATCCTAAA	61759
QY	20811		TCAAGGGTGTCCAAATTTAAATTCAGAGGCCGCTAAATTCAACTAACCTCCCTATTTTC	20870	QY	21891	GATTTCTAGTTCTCTGAGACAGATAAAACCAATAATAATATTTACATACACTCTGGCAAGCAC	21950
Db	60680		TCAAGGGTGTCCAAATTTAAATTCAGAGGCCGCTAAATTCAACTAACCTCCCTATTTTC	60739	Db	61760	GATTTCTAGTTCTGAGACAGATAAAACCAATAATAATATTTACATACACTCTGGCAAGCAC	61819
QY	20871		ATCCCAAGTCTACATCATGGAATAATCCCTCTTTTCTGTCAATCTGAAATTTAGTTTTGC	20930	QY	21951	AACATGGGTGGTGATCAGCTTAAGATAAAATTTAAAAATCTATTTCTTATTTAAAGTGA	22010
Db	60740		ATCCCAAGTCTACATCATGGAATAATCCCTCTTTTCTGTCAATCTGAAATTTAGTTTTGC	60799	Db	61820	AACATGGGTGGTGATCAGCTTAAGATAAAATTTAAAAATCTATTTCTTATTTAAAGTGA	61879
QY	20931		TTTATCAAGCTCTTTGACATCAATTAAGTTTTTTGGGCTCATACAGGCGATTTTCTGG	20990	QY	22011	ACATATTTATTTATTTATACAAAGTTACCTGTCTCGTGGACAGAGT-CAAAATGTGCT	22069
Db	60800		TTTATCAAGCTCTTTGACATCAATTAAGTTTTTTGGGCTCATACAGGCGATTTTCTGG	60859	Db	61880	ACATATTTATTTATTTATACAAAGTTACCTGTCTCGTGGACAGAGTCCAAAATGTGCT	61939
QY	20991		AAAGGCTGGGAAGGCTCCCTGCTCCCAAAACTTCTCTTTGGACATACCTGGTAAAGTGG	21050	QY	22070	TACTGGGTCAAAATCAAGTATGTAAGTAAGTCTGTTTTTGTCAATACAAAAATTCAT	22129
Db	60860		AAAGGCTGGGAAGGCTCCCTGCTCCCAAAACTTCTCTTTGGACATACCTGGTAAAGTGG	60919	Db	61940	TACTGGGTCAAAATCAAGTATGTAAGTAAGTCTGTTTTGTGCAATACAAAAATTCAT	61999
QY	21051		GGGTGCTGCACAGTGCACAGGGGCGCACCTTTCTCTTCTGACGCCCTCTAGGTGCAG	21110	QY	22130	TATGAACAAAAATAATCTCCTCACTTTGAACATGGGAAGCACCTTTGTCTCCACATGC	22189
Db	60920		GGGTGCTGCACAGTGCACAGGGGCGCACCTTTCTCTTCTGACGCCCTCTAGGTGCAG	60979	Db	62000	TATGAACAAAAATAATCTCCTCACTTTGAACATGGGAAGCACCTTTGTCTCCACATGC	62059
QY	21111		CCTAATCAGAGGCTTTTGAGATGTAATAGAATGCTGGGATCTGAGCTCTAGAATGG	21170	QY	22190	ACAATAATTTACTGCTTTGTTGGTCAACAAGAGGATGGTTCCCTGAGTCACTCTCAA	22249
Db	60980		CCTAATCAGAGGCTTTTGAGATGTAATAGAATGCTGGGATCTGAGCTCTAGAATGG	61039	Db	62060	ACAATAATTTACTGCTTTGTTGGTCAACAAGAGGATGGTTCCCTGAGTCACTCTCAA	62119
QY	21171		GGATGTGAATGCACACCCCTTTATAGTTTCTAATATTAGTGTGGGAGGAAGAGATCA	21230	QY	22250	ACATTAAGTTATCAGTTGGCTTTCACCTGCTGGCCATTCATCAATCTTTATCTGTAG	22309
Db	61040		GGATGTGAATGCACACCCCTTTATAGTTTCTAATATTAGTGTGGGAGGAAGAGATCA	61099	Db	62120	ACATTAAGTTATCAGTTGGCTTTCACCTGCTGGCCATTCATCAATCTTTATCTGTAG	62179
QY	21231		ACCTGTTCTTTTGTGATCCGGCCATCTAGACTACTAAGTGCRTGTTCATCATGAGTGA	21290	QY	22310	TAGAAATCATGCTTTTTTCTTCTTGATCATCACAGACTGTGAGAGATCCAAATTAAGT	22369
Db	61100		ACCTGTTCTTTTGTGATCCGGCCATCTAGACTACTAAGTGCRTGTTCATCATGAGTGA	61159	Db	62180	TAGAAATCATGCTTTTTTCTTCTTGATCATCACAGACTGTGAGAGATCCAAATTAAGT	62239
QY	21291		TGAATACATCAATGCTATGAATACATACATCAATTCATCTTACCTTTTCAGTTGAG	21350	QY	22370	GCTGATCTCTCTTGAAGACAGTCACTAATCTTTTTCTTTCTTTCTTTCTTTCTTTG	22429
Db	61160		TGAATACATCAATGCTATGAATACATACATCAATTCATCTTACCTTTTTCAGTTGAG	61219	Db	62240	GCTGATGCTCTTGAAGACAGTCACTAATCTTTTTCTTTCTTTCTTTCTTTCTTTG	62299
QY	21351		GAACTGAGCCCTTTCAAAAGTTTGAAGAAAAAATAAATAAATAAATAAATAAATAA	21410	QY	22430	GACAGAGTCTTCTGCTGCTGCCAGGCTGGAGTGGAGTGGATGATTTTCAGCTCACCATA	22489
Db	61220		GAACTGAGCCCTTTCAAAAGTTTGAAGAAAAAATAAATAAATAAATAAATAAATAA	61279	Db	62300	GACAGAGTCTTCTGCTGCTGCCAGGCTGGAGTGGAGTGGATGATTTTCAGCTCACCATA	62359
QY	21411		CCAGTCAGTGTGAGAGCCAGAGTTTGAATCCAGGCTCTTCATGCTTTTGTACATATG	21470	QY	22490	ACTTCCGCTCCAGGTTTAAAGCAATCTCCGCTCAGCTTCTGAGTAGCTGGGACTA	22549
Db	61280		CCAGTCAGTGTGAGAGCCAGAGTTTGAATCCAGGCTCTTCATGCTTTTGTACATATG	61339	Db	62360	ACTTCCGCTCCAGGTTTAAAGCAATCTCCGCTCAGCTTCTGAGTAGCTGGGACTA	62419
QY	21471		AGCCAGTGTGAAGATTGAAGAGGGTTTCAGAGCAGCTTCCACAGCGATGCTGAAG	21530	QY	22550	CAGGTGCTGCCACATGCCAGCTAATTTTGTATTTTCATTTAGAGATAGAGTTTCACCA	22609
Db	61340		AGCCAGTGTGAAGATTGAAGAGGGTTTCAGAGCAGCTTCCACAGCGATGCTGAAG	61399	Db	62420	CAGGTGCTGCCACATGCCAGCTAATTTTGTATTTTCATTTAGAGATAGAGTTTCACCA	62479
QY	21531		TCTTCCACAGAGGACCACTTGTGTGCAATGACCTGGCTTCTTAGTGGCACCCATAG	21590	QY	22610	TGTTGGCACCACTAATCATTTTATTTGTTTACAAGTCTAGCCCTTATATGCTTAAAGT	22669
Db	61400		TCTTCCACAGAGGACCACTTGTGTGCAATGACCTGGCTTCTTAGTGGCACCCATAG	61459	Db	62480	TGTTGGCACCACTAATCATTTTATTTGTTTACAAGTCTAGCCCTTATATGCTTAAAGT	62539
QY	21591		GCACCTAACCTGTCAATTTTCAATGCTAATTAACATACATACCAAGCAGCAGCTGTG	21650	QY	22670	TCTTTTAACTCTTTAGCAGGATGACAGCAGGCTTACATCTAGTGTGATTTTACCA	22729
Db	61460		GCACCTAACCTGTCAATTTTCAATGCTAATTAACATACATACCAAGCAGCAGCTGTG	61519	Db	62540	TCTTTTAACTCTTTAGCAGGATGACAGCAGGCTTACATCTAGTGTGATTTTACCA	62599
QY	21651		TATCTCATCCACCTATTCAGTTCTGACTAATAAACAGGCGAGCTTTCAGAGTCTACTT	21710	QY	22730	ATGTTGATGGCATGTGGAGAAATGACCACTCAAGTAGGGCCATGATGTTTTTGAAGCA	22789
Db	61520		TATCTCATCCACCTATTCAGTTCTGACTAATAAACAGGCGAGCTTTCAGAGTCTACTT	61579	Db	62600	ATGTTGATGGCATGTGGAGAAATGACCACTCAAGTAGGGCCATGATGTTTTTGAAGCA	62659
QY	21711		TTGTTCTTGGTATGTGATAAAACATTTTGTGCTCTTTTATCTGAACCGAGTGACCTTGGC	21770	QY	22790	TGCTCTTCTTCTTCTGTTTTGCTTCTGTCATCTCAGCTTGTGCTATATTTTAACT	22849
Db	61580		TTGTTCTTGGTATGTGATAAAACATTTTGTGCTCTTTTATCTGAACCGAGTGACCTTGGC	61639	Db	62660	TGCTCTTCTTCTTCTGTTTTGCTTCTGTCATCTCAGCTTGTGCTATATTTTAACT	62719
QY	21771		CAATGCACACTCTCTTTTGTCCCAATTTCTCTTGAACCCCTTTCTTGGCTCATCTAGG	21830	QY	22850	TCTAGAGTCAAGTCAAAAGGCATATTCACCTCTACATCTCTATGACTCTCTCTATGT	22909
Db	61640		CAATGCACACTCTCTCTTTTGTCCCAATTTCTCTTGAACCCCTTTCTTGGCTCATCTAGG	61699	Db	62720	TCTAGAGTCAAGTCAAAAGGCATATTCACCTCTACATCTCTATGACTCTCTCTATGT	62779
QY	21831		AGCTGAATGGATTGATAGCAATGATTTGTCTCAGTGGGAACAAATGCGAGATCCTAAA	21890	QY	22910	ACTCACCACACTTTTCTGCCCCCTATATATAGCATTTACTTCATAGACTCTGTTTGTG	22969
					Db	62780	ACTCACCACACTTTTCTGCCCCCTATATATAGCATTTACTTCATAGACTCTGTTTGTG	62839





Db 65000 ACAGATCAAGAGGAAGTTTAAATCAGAAGCACCCTAAATACTAGAAGGAGCTGAGATTCT 65059  
Qy GTAAATGGTGATTACTAAGGAATAGAAGGCCATGCCACACCTTGAACCTAAATACAAAAGC 25249  
Db GTAAATGGTGATTACTAAGGAATAGAAGGCCATGCCACACCTTGAACCTAAATACAAAAGC 65119  
Qy CAATGATCAGGTGTCCTCAGTTTGAATTTACATCAGAGCTAACACTATCTCTTTGCAAGTGTA 25309  
Db CAATGATCAGGTGTCCTCAGTTTGAATTTACATCAGAGCTAACACTATCTCTTTGCAAGTGTA 65179  
Qy TTAGTCCATTCTCATACTAGATTAAGAAACACCCAGAGCTGGTAGTTTATTAAGAAAA 25369  
Db TTAGTCCATTCTCATACTAGATTAAGAAACACCCAGAGCTGGTAGTTTATTAAGAAAA 65239  
Qy GAGGTTTAATGGCTCACAGTTATGCATTCCTGGAGGCCCTAAGGAAACCTTCAATCAT 25429  
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Qy GGCAGAAAGGCAAGGAAAGCAAGGCACGCTCTTACATGGTGGCAGGAGGAGCATGT 25489  
Db GGCAGAAAGGCAAGGAAAGCAAGGCACGCTCTTACATGGTGGCAGGAGGAGCATGT 65359  
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Db GTGCAAGTGTAGGGAACTGCCCTTTATAAATCATCAGATCTTGTGCCACTCAGTCACT 65419  
Qy ATCACAAGATAGCATGGGAAACCATCCCATGATTCATTAATCTCCATCTTGTCTCT 25609  
Db ATCACAAGATAGCATGGGAAACCATCCCATGATTCATTAATCTCCATCTTGTCTCT 65479  
Qy CCCTTGACATGTGGGATTTATGGGATTTATGGGATTTATGGGATTTATGGGATTTATGGG 25669  
Db CCCTTGACATGTGGGATTTATGGGATTTATGGGATTTATGGGATTTATGGGATTTATGGG 65539  
Qy GGGACACATGATACATATATATAGCAAGTAAAGACACTCAGTGGATCTCTCAG 25729  
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Qy CACACAGGCGCTACAAGCATATATGCTCTAGGAGCAGTGTAGTCTCTTAACTCTA 25789  
Db CACACAGGCGCTACAAGCATATATGCTCTAGGAGCAGTGTAGTCTCTTAACTCTA 65659  
Qy GTGGGGATAAGGAAACCAATCCCATATAATTTTCCAAATGCTTCAAGAAAAAATTA 25849  
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Qy CCTATTGATTTGATTTGAATGACATGCCCTAGATGAGGGGAATTAACCTTTGATAATGAGG 26029  
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Qy TGGGGTTAGGATATCCACAAGACGCAACACTCGCTCTAGGATGAAGCAGAGGTGGCAC 26089  
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Qy AGGCACAGGAGGAAAAACAACTGAAAGTTGTCCCACTGCTGAGATTTTCTTAAATATT 26149  
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Qy TCATGTGTGTGCCCTCATAGACACACAAATATGATAAACAACAATATGTTTTTATGAA 26209  
Db TCATGTGTGTGCCCTCATAGACACACAAATATGATAAACAACAATATGTTTTTATGAA 66079  
Qy TGCCTTCTGGCAACACAGTAACTGAGGAGCTAGATCTTACAATCATATGAGTCATA 26269  
Db TGCCTTCTGGCAACACAGTAACTGAGGAGCTAGATCTTACAATCATATGAGTCATA 67219

Db 66080 TGCTTGTGCGCAACAGAGTAAGTGAGGCGAGCTAGACTACTTACAAATCATATGAGTCATA 66139  
Qy AACAGTGGCAAAAAGTCTCTAAAAAGAAAAGCTTAGCAGAAAAACATCCAAATAGACAAAAT 26329  
Db AACAGTGGCAAAAAGTCTCTAAAAAGAAAAGCTTAGCAGAAAAACATCCAAATAGACAAAAT 66199  
Qy AGTGTGAGAAAAATTTCTGGATAAATAGTATCAGAAAAAGTTTACTACTTGGAGATAATTTT 26389  
Db AGTGTGAGAAAAATTTCTGGATAAATAGTATCAGAAAAAGTTTACTACTTGGAGATAATTTT 66259  
Qy GAAAACTTTTAATGAGTACACTGATTTATACAGATAATTAATTAAGACAATATTGGCAAA 26449  
Db GAAAACTTTTAATGAGTACACTGATTTATACAGATAATTAATTAAGACAATATTGGCAAA 66319  
Qy TACTATCTGTGAGGCTCTCCAGATTTACTGATGGTTATCTTAGAGCCCTTATAGGGAAGACA 26509  
Db TACTATCTGTGAGGCTCTCCAGATTTACTGATGGTTATCTTAGAGCCCTTATAGGGAAGACA 66379  
Qy GCAGACAATTAATAGAAATATCTTGGTTCTGTGCAGAGTTTTCGAAGCAATTTCAAATAA 26569  
Db GCAGACAATTAATAGAAATATCTTGGTTCTGTGCAGAGTTTTCGAAGCAATTTCAAATAA 66439  
Qy TAACAGTACTATCATTTTATGAGGCTGTAGATCTCTTCAATACCTAATCCTAACAC 26629  
Db TAACAGTACTATCATTTTATGAGGCTGTAGATCTCTTCAATACCTAATCCTAACAC 66499  
Qy AAATTTGCAAGTGCTTATAAATTTAGAGCCATTTTACAAAAGAGAAAATAGAGAACTCAG 26689  
Db AAATTTGCAAGTGCTTATAAATTTAGAGCCATTTTACAAAAGAGAAAATAGAGAACTCAG 66559  
Qy GGGTCTGTAAAGTACTTCTCCAAAGGCCACTGCTACTGATTTTAGGATTTGAGTTAGAAAT 26749  
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Qy TTATTTACAGTTTAGTTTGGTCTCTCAAGTCCAGTCTCTTCCACTGCAAGCTCTCTTTC 26809  
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Db CACTTGGTAAAGGTACCAAATATACCACATGGTTCCAGGAACCTCAATGAAGCTAACCATC 66799  
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Qy AATTTCTTACCCCAAGTATCAAAATAGCAGAGAAAATTCGACGCACTCAGTTTCTAA 27169  
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Qy AATATGTTTCATATGTTAATGCTCTCTGAAATAATTTCTTCAATTTGAAATCATTTTGA 27229  
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Db AATCAAACTTGTGCTCTCTGTTTAGCATGCGATGGCATGACAAAGAAACAGCAATAA 67159  
Qy TCATAAAAATTTTTTAAAGAACCTTCTGACTTAAAGAACTCAGAGAAATGAACA 27349  
Db TCATAAAAATTTTTTAAAGAACCTTCTGACTTAAAGAACTCAGAGAAATGAACA 67219



QY	27350	TACTGATATAAACAAATTTATTTTCAATTTATTTCTCAGTTCTTCTATGCTAGTCTATTTACCTG	27409	28430	GTTTGTACATATATATACATGTGCCATGTGTGGTGTGCTGCACCCCAATTAACCTGTCATTT	28489
Db	67220	TACTGATATAAACAAATTTATTTTCAATTTATTTCTCAGTTCTTCTATGCTAGTCTATTTACCTG	67279	68300	GTTTGTACATATATATACATGTGCCATGTGTGGTGTGCTGCACCCCAATTAACCTGTCATTT	68359
QY	27410	TAAATAATTTGCAAAATAGAGTCAAAATGTTTATAGATTTTAGAGGAAAATGTCATGGAGAA	27469	28490	ACATTTAGGTATATCTCTTAATGCTATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT	28549
Db	67280	TAAATAATTTGCAAAATAGAGTCAAAATGTTTATAGATTTTAGAGGAAAATGTCATGGAGAA	67339	68360	AAATTTAGGTATATCTCTTAATGCTATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT	68419
QY	27470	AATAATAGAAATTTGGTATAGATCTCTTGAAGTGGTGTGTAAGTGTCCACAGTGTCTAAC	27529	28550	CAGTGTGTCATGTTCCTCTCTGTCATGTTCTCTCATTTCTCTCATTTCTCTCATTTCTCTCAT	28609
Db	67340	AATAATAGAAATTTGGTATAGATCTCTTGAAGTGGTGTGTAAGTGTCCACAGTGTCTAAC	67399	68420	CAGTGTGTCATGTTCCTCTCTGTCATGTTCTCTCATTTCTCTCATTTCTCTCATTTCTCTCAT	68479
QY	27530	ATCTAACCAATTTAGAGTCTGTAAAAATACATATTTCAACGTCATCATTTTGGAACTAAT	27589	28610	AGTGAGAACATCGGGTGTGTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	28669
Db	67400	ATCTAACCAATTTAGAGTCTGTAAAAATACATATTTCAACGTCATCATTTTGGAACTAAT	67459	68480	AGTGAGAACATCGGGTGTGTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	68539
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1 (bases 1 to 160345)  
Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
Homo sapiens chromosome 11, clone RP11-475J2  
Unpublished  
2 (bases 1 to 160345)  
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bedalov,F.,  
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,  
Campoliano,A., Castelle,A., Choepe,Y., Colangelo,M., Collins,S.,  
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Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
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Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,  
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Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,  
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
Young,G., Zainoun,J., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (27-APR-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jun 23, 2000 this sequence version replaced gi:8099852.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Project name: L8810  
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----- Summary Statistics  
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Chemistry: Dye-terminator Big Dye; 100% of reads  
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Library size: 158645; sum-of-contigs  
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Quality coverage: 5.0 in Q20 bases; sum-of-contigs  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 18 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
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SEQUENCE, 18 unordered pieces.
AC067870
VERSION AC067870.3 GI:8671974
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SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-475J2
Unpublished
2 (bases 1 to 160345)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
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Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
TITLE Submitted (27-APR-2000) Whitehead Institute/MIT Center for Genome
JOURNAL Research, 320 Charles Street, Cambridge, MA 02141, USA
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## COMMENT

On Jun 23, 2000 this sequence version replaced gi:8099852.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
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Genome Center  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
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Center clone name: 475\_J2  
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Chemistry: Dye-terminator Big Dye; 100% of reads  
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Insert size: 158645; sum-of-contigs  
Quality coverage: 4.9 in Q20 bases; agarose-fp  
Quality coverage: 5.0 in Q20 bases; sum-of-contigs  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 18 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence.  
\* as soon as it is available and the accession number will  
\* be preserved.

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Db  
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Db	38183	CCCTTTAAGGAAATCACTACCCAAATATATCTTTTATATCTATGATGGGTTTCAGGACA	38242	Db	39263	TATTAGCTTCGTTAGAAAGCTTTCCAGTTTCCAGATTTAAATTCCTTAAAGGTTGAGCACT	39322
QY	13181	CTGTACTCCCAATGTTTTAAGCTGAAGAAATTTGAGAAACAAGAAAGCAGAAAGATC	13240	QY	14261	GAAATATTTGTTGGAGAAATCACAAAGGCTGTTATGTGACAAGGTTCTCATTTACCCCTTAA	14320
Db	38243	CTGTACTCCCAATGTTTTAAGCTGAAGAAATTTGAGAAACAAGAAAGCAGAAAGATC	38302	Db	39323	GAAATATTTGTTGGAGAAATCACAAAGGCTGTTATGTGACAAGGTTCTCATTTACCCCTTAA	39382
QY	13241	ACTCTGACCTTCCCTCACCCCTCATCTGAAGGAAGTCATAAAACCTAGGATTTCTGA	13300	QY	14321	GGTGTCTCATCTTTCCAGAAACCTCATTTACATCTCATCATGTTGCAACCATGAGCTGGG	14380
Db	38303	ACTCTGACCTTCCCTCACCCCTCATCTGAAGGAAGTCATAAAACCTAGGATTTCTGA	38362	Db	39383	GGTGTCTCATCTTTCCAGAAACCTCATTTACATCTCATCATGTTGCAACCATGAGCTGGG	39442
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QY	13361	GAAAGAGAATTCCTCCCGGCTTTTGTGAGATGTGCTTACTCTGTCACCCAGGC	13420	QY	14441	TAGAAATTTTCCCTTAATGAGACTAGGCTCAAGCAACCCCTTCTGGAATGGAATAAG	14500
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QY	13601	GCTATGTTGACCGTGTGATCTGAACCTCATAGCTCAAGGATCATCCCACTTGGCT	13660	QY	14681	GCAGAGTCTAGAAAGTAAAAATATTAGGACACATGTCTTAAAGAGATGCTTTAGATACAG	14740
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Db	41482	AGAGCTGCTGCCTATGTCACGGAAGAGCTTAACCTCTCTTTCAGTCTACTCTCTCTCT	41539
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DEFINITION			
ACCESSION	AK025378		
VERSION	AK025378.1 GI:10437881		
KEYWORDS	oligo capping; fis (full insert sequence).		
SOURCE	Homo sapiens colon mucosa cDNA to mRNA, clone_lib:ColF		
	clone:COLF1013.		
ORGANISM	Homo sapiens		
REFERENCE	1 (sites) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Tashiro,H., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura,Y.		
TITLE	Submitted (29-AUG-2000) Sumlo Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdna@leims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)		
JOURNAL	NEDO human cDNA sequencing project		
REFERENCE	2 (bases 1 to 1149)		
AUTHORS	Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura,Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (29-AUG-2000) Sumlo Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdna@leims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)		
COMMENT	NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing; Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).		
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Qy	11363	GCCTGATCTGAAGCTAGATTGAGAGGAGGAGGTGTCAGCTTTGTATATCTTTAAACAAG	11422
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Qy	16180	TCAACAGTAATTCCTAACAATGATGTTGCTTCATATTTTATGTTTATAATTTAAACAT	16239
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Qy	16240	ATTTCCTGATGATGTTTAACTCTTGCAAAATATATTTTCATATGATTTATTTTATGAC	16299
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Qy	16300	CCTCAGAGCAACTCTGGAAGGGTTATCTGATATATTAATTTTTCAGTCTTATTTAAATA	16359
Db	41362	CCTCAGAGCAACTCTGGAAGGGTTATCTGATATATTAATTTTTCAGTCTTATTTAAATA	41421
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RESULT 6
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DEFINITION Sequence 3 from Patent WO0125437.
ACCESSION AX164746
VERSION AX164746.1 GI:14545599
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1587)
Shinkets,R.A., Lichenstein,H., Herrmann,J.L., Boldog,F.L.,
Minskoff,S. and Jeffers,M.
Growth factor polypeptides and nucleic acids encoding same
TITLE Patent: WO 0125437-A 3 12-APR-2001;
JOURNAL Curagen Corporation (US)
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VERSION AX164761.1 GI:14545604
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AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1734)
Shinkets,R.A., Lichenstein,H., Herrmann,J.L., Boldog,F.L.,
Minskoff,S. and Jeffers,M.
Growth factor polypeptides and nucleic acids encoding same
TITLE Patent: WO 0125437-A 18 12-APR-2001;
JOURNAL Curagen Corporation (US)
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LOCUS AX164744 1828 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1 from Patent WO0125437.
ACCESSION AX164744
VERSION AX164744.1 GI:14545598
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1828)
AUTHORS Shimkets, R.A., Lichenstein, H., Herrmann, J.L., Boldog, F.L.,
Minskoff, S., and Jeffers, M.
TITLE Growth factor polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0125437-A 1 12-APR-2001;
Curagen Corporation (US)
FEATURES
source
1. .1828
Location/Qualifiers
/organism="Homo sapiens"
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BASE COUNT 572 a 380 c 385 g 491 t
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Best Local Similarity 100.0%; Pred. No. 2.2e-310;
Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS AF335584 1828 bp mRNA linear PRI 24-APR-2001
DEFINITION Homo sapiens platelet-derived growth factor D mRNA, complete cds.
ACCESSION AF335584
VERSION AF335584.1 GI:13774335
KEYWORDS
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1828)
AUTHORS Laroche, W.J., Jeffers, M., McDonald, W.F., Chiklaku, R.A.,
Giese, M., Sulkowicz, N., Sulkowicz, G., Boldog, F.L., Yang, M.,
Vernet, C., Burgess, C., Fernandez, E., Deegler, L.L., Rittman, B.,
Shimkets, J., Shimkets, R., Lichenstein, H., and Lichenstein, H.S.
TITLE PDGF-D, a new protease-activated growth factor
JOURNAL Nat. Cell Biol. 3 (5): 517-521 (2001)
MEDLINE 21231380
PUBMED 11331882
REFERENCE 2 (bases 1 to 1828)
AUTHORS Laroche, W.J., Jeffers, M., Yang, M., Vernet, C., Burgess, C.E.,
Fernandez, E., Shimkets, R.A. and Lichenstein, H.S.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (11-JAN-2001) Development, Curagen Corporation, 322 East
Main Street, Branford, CT 06405, USA
FEATURES
Location/Qualifiers
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182. .1294
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LOCUS
DEFINITION
Sequence 1 from Patent WO0189450.
ACCESSION
AX365305
VERSION
AX365305.1 GI:18697036
KEYWORDS
human.
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Beals, J.M., Gonzalez-Dewhitt, P.A., Hammond, L.J., Lu, J., Na, S.,
Su, E.W., Witcher, D.R. and Wroblewski, V.J.
TITLE
Treating musculoskeletal disorders using lp85 and analogs thereof
JOURNAL
Patent WO0189450-A. 1. 29-NOV-2001;
ELI LILLY AND COMPANY (US)
FEATURES
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114..149
BASE COUNT 1164 a 736 c 718 g 1118 t
ORIGIN
Query Match 2.2%; Score 652; DB 6; Length 3736;
Best Local Similarity 100.0%; Pred. No. 2e-310;
Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1750 GTATATGTAAGAAAGCCTCATCTTTTGATTTTATATACAGAGCTTCTTTTAAGAGA 1691
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BC030645 4070 bp mRNA linear PRI 21-MAY-2002
Homo sapiens, spinal cord-derived growth factor-B, clone MGC:26867
IMAGE:4824526, mRNA, complete cds.
BC030645
ACCESSION BC030645
VERSION BC030645
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4070)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (20-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 33 Row: 1 Column: 12
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 15451919.
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BASE COUNT 1227 a 843 c 831 g 1169 t
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## ORIGIN

Query Match	2.2%	Score 652	DB 9	Length 4070
Best Local Similarity	100.0%	Pred. No. 28-310		
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DB	2076	GTATATGTAAGAAGCCTCATCTTTTGATTTTAAATATACAAGATGCTTCTTTAAGAGA	2017	
QY	61	GCAAGATTCAAAATGTGTTTGTGTTCCAAAATTTAAAAATTAATATCTCCTAAATTTT	120	
DB	2016	GCAAGATTCAAAATGTGTTTGTGTTCCAAAATTTAAAAATTAATATCTCCTAAATTTT	1957	
QY	121	CTAAGACATGTTTCATATATTTGACATCCCTTATTTGGCAAGAGATTTTAAGAGTCT	180	
DB	1956	CTAAGACATGTTTCATATATTTGACATCCCTTATTTGGCAAGAGATTTTAAGAGTCT	1897	
QY	181	AACTCAAAACATATGTAAAGCTCTGGTGACCTGGTTATATATACCAAAAAAACAATTTGAT	240	
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QY	361	TTGCCATGGCATTAACAAGCAGGCTGAGACTCAGCAACCACTTGTTGTTCAATGCATG	420	
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DB	1596	ACTAAAGGTTCTTTTCAGGCTTAATGTAAAGATGTGCACATTTCTTTATCAGAGTGGTCTT	1537	
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RESULT	13
LOCUS	AF336376/c
DEFINITION	AF336376 Homo sapiens platelet-derived growth factor D (PDGFD) mRNA, complete cds.
ACCESSION	AF336376
VERSION	AF336376.1 GI:14193795
KEYWORDS	.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens

REFERENCE 1 (bases 1 to 2253)  
AUTHORS Bergsten, E., Uutela, M., Li, X., Pietras, K., Ostman, A., Heldin, C. H., Allitalo, K., and Eriksson, U.  
TITLE pter-D is a specific, protease-activated ligand for the PDGF beta-receptor  
JOURNAL Nat. Cell Biol. 3 (5), 502-516 (2001)  
MEDLINE 24231375  
PUBMED 11331881  
REFERENCE 2 (bases 1 to 2253)  
AUTHORS Bergsten, E., Uutela, M., Li, X., Pietras, K., Ostman, A., Heldin, C. H.,

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Alitalo,K. and Erkksson,U.
Direct Submission
Submitted (15-JAN-2001) Ludwig Institute for Cancer Research,
Nobelisvag 3 (Box 240), Stockholm S-171 77, Sweden
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701 a 464 c 490 g 598 t
BASE COUNT
ORIGIN

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Db	1332	ACTAAAGGTTCTTTCAGGCTTAATGTTAAGATGTGCACATCTCTTATCAGGTGGTCTT	1273				



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Db 1212 GCTTACGCTCTACCCCTCTCTGATGTGGCGAGGCTCAAACTGTAATACCT 1161  
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RESULT 14  
AY027518/c 3710 bp mRNA linear PRI 17-JUL-2002  
LOCUS Homo sapiens iris-expressed growth factor short form (IEGF) mRNA,  
DEFINITION complete cds, alternatively spliced.  
ACCESSION AY027518  
VERSION AY027518.1 GI:13432062  
KEYWORDS  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1. (bases 1 to 3710)  
AUTHORS Wistow,G., Berstein,S.L., Ray,S., Wyatt,M.K., Behal,A.,  
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.

Expressed-sequence tag analysis of adult human iris for the NEIBank  
Project: steroid response factors and similarities with retinal  
pigment epithelium  
JOURNAL Mol. Vis. 8, 185-195. (2002)  
MEDLINE 22103462  
PUBMED 12107412

REFERENCE 2 (bases 1 to 3710)  
AUTHORS Wistow,G.  
TITLE Direct Submission  
JOURNAL Submitted (13-FEB-2001) MSF, NEI, 6/331, NIH, Bethesda, MD  
20892-2740, USA

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BASE COUNT 1169 a 724 c 703 g 1114 t  
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Best Local Similarity 99.7%; Pred. NO. 5.6e-260;  
Matches 650; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 181 RACTCAACATATGTAAGCTCTGGTGTACCTGGTTATATATACCAAAAACATTTGAT 240  
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QY 361 TTGCCATGGCATTACAAGCAAGGCTGAGACTCAGCAACCACTTGTGTTGATTCATG 420  
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LOCUS Homo sapiens iris-expressed growth factor long form (IEGF) mRNA,  
DEFINITION complete cds, alternatively spliced.  
ACCESSION AY027517  
VERSION AY027517.1 GI:13432060  
KEYWORDS  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1. (bases 1 to 3729)  
AUTHORS Wistow,G., Berstein,S.L., Ray,S., Wyatt,M.K., Behal,A.,  
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.

Expressed-sequence tag analysis of adult human iris for the NEIBank  
Project: steroid response factors and similarities with retinal  
pigment epithelium  
JOURNAL Mol. Vis. 8, 185-195. (2002)  
MEDLINE 22103462  
PUBMED 12107412

REFERENCE 2 (bases 1 to 3729)  
AUTHORS Wistow,G.  
TITLE Direct Submission  
JOURNAL Submitted (13-FEB-2001) MSF, NEI, 6/331, NIH, Bethesda, MD  
20892-2740, USA

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93. 1205  
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CDS



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TYEDLLKYNPESWQEDLENWILDTPRYGRSHDRKSKVDLDRLNDKARYSCTERN  
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BASE COUNT	1177 a	730 c	706 g	1116 t
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Best Local Similarity	99.7%;	Pred. No. 5.8e-260;		
Matches 650;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
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Qy	121	CTAAGACATGTTTCATATATTTTGACCATCCCTTATTTGGCAAGAGATTTTAAGAGTCT	180	
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Qy	541	GAGCTGCAGATACAAATCACATCGTTTATGTGTATGATGATGATGATGATGATGATGATG	600	
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Qy	601	GTCTTAGCTCTACCCCTCCCTCTTGTATGTGGCCAGGCTCAAACTGTAATACCT	652	
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2003, 06:57:06 : Search time 865 Seconds

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US-10-083-853b-2

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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C 2	300	1.0	1910	US-09-457-066-36	Sequence 36, Appl
C 3	119	0.4	33042	US-09-245-281-44	Sequence 44, Appl
C 4	103	0.3	18596	US-09-318-448-11	Sequence 11, Appl
C 5	94	0.3	50000	US-09-146-053-4	Sequence 4, Appl
C 6	91	0.3	33042	US-09-245-281-44	Sequence 44, Appl
C 7	91	0.3	152331	US-09-128-155-16	Sequence 16, Appl
C 8	91	0.3	168575	US-09-426-290-1	Sequence 1, Appli
C 9	87	0.3	176373	US-08-128-155-17	Sequence 17, Appl
C 10	87	0.3	40328	US-08-742-185-102	Sequence 102, App
C 11	83	0.3	10754	US-08-966-958-1	Sequence 1, Appli
C 12	83	0.3	10754	US-09-215-817-1	Sequence 1, Appli
C 13	83	0.3	10754	US-09-342-353-1	Sequence 1, Appli
C 14	80	0.3	6623	US-08-687-080-68	Sequence 68, Appl
C 15	78	0.3	797	US-08-592-126-73	Sequence 73, Appl
C 16	78	0.3	10607	US-08-078-090-3	Sequence 3, Appli
C 17	73	0.2	731	US-09-288-143-38	Sequence 38, Appl
C 18	71	0.2	98844	US-09-791-211-10	Sequence 10, Appl
C 19	69	0.2	623	US-09-385-962-167	Sequence 167, Appl
C 20	64	0.2	87350	US-08-781-891-79	Sequence 79, Appl
C 21	64	0.2	87543	US-09-791-211-3	Sequence 3, Appli
C 22	64	0.2	168575	US-09-426-290-1	Sequence 1, Appli
C 23	63	0.2	112132	US-09-741-150-3	Sequence 3, Appli
C 24	60	0.2	225	US-09-397-787-117	Sequence 117, App
C 25	59	0.2	43795	US-08-742-185-101	Sequence 101, App
C 26	57	0.2	40328	US-08-742-185-102	Sequence 102, App
C 27	56	0.2	482	US-08-991-789A-246	Sequence 246, App

28	56	0.2	482	4	US-09-062-451-246	Sequence 246, App
29	56	0.2	482	4	US-09-598-326-246	Sequence 246, App
30	56	0.2	6623	2	US-08-687-080-68	Sequence 68, Appl
31	55	0.2	439	4	US-09-397-787-269	Sequence 269, App
32	55	0.2	7452	3	US-08-592-500-1	Sequence 1, Appli
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34	55	0.2	7452	5	PCT-US94-07644A-1	Sequence 11, Appli
35	55	0.2	18596	4	US-09-318-448-11	Sequence 11, Appli
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37	54	0.2	430	4	US-09-397-787-248	Sequence 248, App
38	54	0.2	573	4	US-09-385-982-420	Sequence 420, App
39	54	0.2	2087	4	US-09-097-199-63	Sequence 83, Appl
40	54	0.2	13187	4	US-09-422-936-61	Sequence 61, Appl
41	54	0.2	72928	3	US-09-009-913-1	Sequence 1, Appli
42	53	0.2	1523	1	US-07-795-859B-25	Sequence 25, Appl
43	53	0.2	1523	1	US-08-457-616-25	Sequence 25, Appl
44	53	0.2	4072	4	US-09-245-041-16	Sequence 16, Appl
45	53	0.2	38844	4	US-09-734-675-3	Sequence 3, Appli

## ALIGNMENTS

RESULT 1  
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Sequence 1, Application US/09540224  
Patent No. 6468543  
GENERAL INFORMATION:  
APPLICANT: Gilbertson, Debra G.  
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
FILE REFERENCE: 00-28  
CURRENT APPLICATION NUMBER: US/09/540,224  
CURRENT FILING DATE: 2000-03-31  
EARLIER APPLICATION NUMBER: US 60/180,169  
EARLIER FILING DATE: 2000-02-04  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 1882  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (226)...(1338)  
US-09-540-224-1  
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Matches 427; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
1.3%; Score 377; DB 4; Length 1882;  
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Db 1278 GTCACATGAGCATGCTTGTAGCTACCCCTCTCTGATGTCGCGAGGCTCAACTG 1219
Oy 645 TAATACCT 652
Db 1218 TAATACCT 1211
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## RESULT 2

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US-09-457-066-36/c
; Sequence 36, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 1862
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (226)...(1338)
US-09-457-066-36
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Db 1486 TGTGTCTACTTGCATGCGCTAGTAGTAGTGTGTTGCTGTGAGAAAAGGCTCTCT 1427
Oy 465 ATCTACAGCTCTTAACATAAGGTTCTTTCAGGCTTAATGAGATGTCACATCTC 524
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## RESULT 3

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US-09-245-281-44
; Sequence 44, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
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; CURRENT APPLICATION NUMBER: US/09/245,281
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/039,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 32042
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-245-281-44
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Best Local Similarity 100.0%; Pred. No. 7.9e-30;
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Db 13428 AAGATCAGATAGTTGTAGATATGCGGCAATTTCTGAGGCTGTGTTGCATG 13486
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## RESULT 4

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US-09-318-448-11
; Sequence 11, Application US/09318448
; Patent No. 6210950
; GENERAL INFORMATION:
; APPLICANT: Johnson, William G.
; APPLICANT: Steiros, Edward S.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
; FILE REFERENCE: 601-1-057
; CURRENT APPLICATION NUMBER: US/09/318,448
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 18596
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-318-448-11
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Best Local Similarity 100.0%; Pred. No. 1.2e-24;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 29385 GATCCCATTTGTCAATTTTGGCTTTGTGCGATTCGTTTGG 29427
Db 6766 GATCCCATTTGTCAATTTTGGCTTTGTGCGATTCGTTTGG 6808
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## RESULT 5

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US-09-146-053-4
; Sequence 4, Application US/09146053A
; Patent No. 6399349
; GENERAL INFORMATION:
; APPLICANT: Ryan, James W.
; APPLICANT: Sprinkle, Terry Joe Curtis
; APPLICANT: Venema, Richard C.
; TITLE OF INVENTION: Human Aminopeptidase P Gene
; FILE REFERENCE: MCG103
; CURRENT APPLICATION NUMBER: US/09/146,053A
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; CURRENT FILING DATE: 1998-09-02  
; EARLIER APPLICATION NUMBER: 60/057,854  
; EARLIER FILING DATE: 1997-09-02  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 50000  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-146-053-4

Query Match 0.3%; Score 94; DB 4; Length 50000;  
Best Local Similarity 100.0%; Pred. No. 8e-22;  
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 29497 TTTTATGTTTAAAGTCTTAAGTCTTTAATCCATCTTGAATTAATTTTGTATA 29556  
Db 27116 TTTTATGTTTAAAGTCTTAAGTCTTTAATCCATCTTGAATTAATTTTGTATA 27175  
QY 29557 AGGTGAAGGAAGGATCCAGTTTCAGCTTTCTA 29590  
Db 27176 AGGTGAAGGAAGGATCCAGTTTCAGCTTTCTA 27209

## RESULT 6

US-09-245-281-44/c  
; Sequence 44, Application US/09245281  
; Patent No. 6369196  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
; FILE REFERENCE: 07334/118001  
; CURRENT APPLICATION NUMBER: US/09/245,281  
; CURRENT FILING DATE: 1999-02-05  
; EARLIER APPLICATION NUMBER: US 09/207,359  
; EARLIER FILING DATE: 1998-12-08  
; EARLIER APPLICATION NUMBER: US 09/099,041  
; EARLIER FILING DATE: 1998-06-17  
; EARLIER APPLICATION NUMBER: US 09/019,942  
; EARLIER FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 44  
; LENGTH: 32042  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-245-281-44

Query Match 0.3%; Score 91; DB 4; Length 32042;  
Best Local Similarity 100.0%; Pred. No. 7.9e-21;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 15964 GCAGGGTTCGATCTCTGTGATAAAACAGCTTTAAACCAACAAAGATCAAAAGA 15905  
QY 3704 GACAAAGAGCCATTACATAATGGTTAAAG 3734  
Db 15904 GACAAAGAGCCATTACATAATGGTTAAAG 15874

## RESULT 7

US-09-128-155-16  
; Sequence 16, Application US/09128155  
; Patent No. 6117654  
; GENERAL INFORMATION:  
; APPLICANT: Pan, Yanq  
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
; FILE REFERENCE: 09404/052001  
; CURRENT APPLICATION NUMBER: US/09/128,155  
; CURRENT FILING DATE: 1998-08-03

; EARLIER APPLICATION NUMBER: US 60/091,650  
; EARLIER FILING DATE: 1998-07-02  
; EARLIER APPLICATION NUMBER: US 60/054,646  
; EARLIER FILING DATE: 1997-08-04  
; NUMBER OF SEQ ID NOS: 18  
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; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(152331)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-128-155-16

Query Match 0.3%; Score 91; DB 3; Length 152331;  
Best Local Similarity 100.0%; Pred. No. 6.1e-21;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 28846 TGTGTCTTTATAGCAGCATGATTATATCCTTTGGGTATATACCCAGTAATGGATGGC 28905  
Db 53689 TGTGTCTTTATAGCAGCATGATTATATCCTTTGGGTATATACCCAGTAATGGATGGC 53748  
QY 28906 TGGTCAAATGGTATTCTTAGTCTTAGATCC 28936  
Db 53749 TGGTCAAATGGTATTCTTAGTCTTAGATCC 53779

## RESULT 8

US-09-426-290-1/c  
; Sequence 1, Application US/09426290  
; Patent No. 6410712  
; GENERAL INFORMATION:  
; APPLICANT: Berglind Ran Olafsdottir  
; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE  
; FILE REFERENCE: 2345.2001-000  
; CURRENT APPLICATION NUMBER: US/09/426,290  
; CURRENT FILING DATE: 1999-10-25  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 168575  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (21181)...(21403)  
; NAME/KEY: CDS  
; LOCATION: (95252)...(95430)  
; NAME/KEY: CDS  
; LOCATION: (101753)...(101996)  
; NAME/KEY: CDS  
; LOCATION: (110324)...(110439)  
; NAME/KEY: CDS  
; LOCATION: (124058)...(124278)  
; NAME/KEY: CDS  
; LOCATION: (127009)...(127130)  
; NAME/KEY: CDS  
; LOCATION: (128910)...(129139)  
US-09-426-290-1

Query Match 0.3%; Score 91; DB 4; Length 168575;  
Best Local Similarity 100.0%; Pred. No. 6e-21;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3644 GCAGGGTTCGATCTCTGTGATAAAACAGCTTTAAACCAACAAAGATCAAAAGA 3703  
Db 156614 GCAGGGTTCGATCTCTGTGATAAAACAGCTTTAAACCAACAAAGATCAAAAGA 156555  
QY 3704 GACAAAGAGCCATTACATAATGGTTAAAG 3734

Db 156554 GACAAAGAGGCCATTACATAATGGTAAAGG 156524

## RESULT 9

US-09-128-155-17  
; Sequence 17, Application US/09128155  
; Patent No. 6117654  
; GENERAL INFORMATION:  
; APPLICANT: Pan, Yang  
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: 09404/052001  
; CURRENT APPLICATION NUMBER: US/09/128,155  
; EARLIER FILING DATE: 1998-08-03  
; EARLIER APPLICATION NUMBER: US 60/091,650  
; EARLIER FILING DATE: 1998-07-02  
; EARLIER APPLICATION NUMBER: US 60/054,646  
; EARLIER FILING DATE: 1997-08-04  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 176373  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(176373)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-128-155-17

Query Match 0.3%; Score 91; DB 3; Length 176373;

Best Local Similarity 100.0%; Pred. No. 5.9e-21;

Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28846 TGTGCTTTATAGCAGCATGATTATATCCCTTTGGGTATATACCCAGTAATGGGATGCC 28905

Db 56333 TGTGCTTTATAGCAGCATGATTATATCCCTTTGGGTATATACCCAGTAATGGGATGCC 56392

QY 28906 TGGGTCATGTTTCTAGTCTAGATCC 28936

Db 56393 TGGGTCATGTTTCTAGTCTAGATCC 56423

## RESULT 10

US-08-742-185-102  
; Sequence 102, Application US/08742185  
; Patent No. 6020476  
; GENERAL INFORMATION:  
; APPLICANT: Page, David C.  
; APPLICANT: Reijo, Renee  
; APPLICANT: Saxena, Richa  
; APPLICANT: Hawkins, Trevor  
; APPLICANT: Reeve, Mary Pat  
; TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA  
; NUMBER OF SEQUENCES: 102  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: US  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/742,185  
; FILING DATE: 30-OCT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/690,734

; FILING DATE: 31-JUL-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/310,429  
; FILING DATE: 22-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: WHI94-07A2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 102:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40328 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-742-185-102

Query Match 0.3%; Score 87; DB 3; Length 40328;

Best Local Similarity 100.0%; Pred. No. 1.5e-19;

Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29612 CAGCACCATTTTAAATAGGAATCCTTTCCCATTCGTTGTTTCTCAGGTTGTCA 29671

Db 17587 CAGCACCATTTTAAATAGGAATCCTTTCCCATTCGTTGTTTCTCAGGTTGTCA 17646

QY 29672 AGATCAGATAGTTGTAGATATGCGGC 29698

Db 17647 AGATCAGATAGTTGTAGATATGCGGC 17673

## RESULT 11

US-08-966-958-1/C  
; Sequence 1, Application US/08966958  
; Patent No. 5928908  
; GENERAL INFORMATION:  
; APPLICANT: Dunn, John  
; APPLICANT: Randesi, Matthew  
; TITLE OF INVENTION: METHODS FOR INTRODUCING UNIDIRECTIONAL  
; TITLE OF INVENTION: DELETIONS  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brookhaven National Laboratory  
; STREET: P.O. Box 5000  
; CITY: Upton  
; STATE: New York  
; COUNTRY: US  
; ZIP: 11973  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/966,958  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bogosian, Margaret  
; REGISTRATION NUMBER: 25,324  
; REFERENCE/DOCKET NUMBER: AUI97-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 344-3341  
; TELEFAX: (516) 344-3729  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10754 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)

US-08-966-958-1

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Best Local Similarity 100.0%; Pred. No. 3.5e-18;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 10716 CAGCACCATTTAATAATAGGAATCCTTTCCCATTCGTTGTTTCTCAGGTTTGTC 10657  
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QY 29672 AGATCAGATAGTTGTAGATATG 29694  
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Db 10656 AGATCAGATAGTTGTAGATATG 10634  
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RESULT 12

US-09-215-817-1/c

; Sequence 1, Application US/09215817

; Patent No. 5968786

; GENERAL INFORMATION:

; APPLICANT: Dunn, John

; APPLICANT: Randesi, Matthew

; TITLE OF INVENTION: METHODS FOR INTRODUCING UNIDIRECTIONAL

; DELETIONS

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brookhaven National Laboratory

; STREET: P.O. Box 5000

; CITY: Upton

; STATE: New York

; COUNTRY: US

; ZIP: 11973

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/215,817

; FILING DATE:

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/966,958

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Bogosian, Margaret

; REGISTRATION NUMBER: 25,324

; REFERENCE/DOCKET NUMBER: AUI97-14

; TELEPHONE: (516) 344-3341

; TELEFAX: (516) 344-3729

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10754 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-09-215-817-1

Query Match 0.3%; Score 83; DB 2; Length 10754;  
Best Local Similarity 100.0%; Pred. No. 3.5e-18;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29612 CAGCACCATTTAATAATAGGAATCCTTTCCCATTCGTTGTTTCTCAGGTTTGTC 29671  
|||||  
Db 10716 CAGCACCATTTAATAATAGGAATCCTTTCCCATTCGTTGTTTCTCAGGTTTGTC 10657  
|||||

QY 29672 AGATCAGATAGTTGTAGATATG 29694  
|||||  
Db 10656 AGATCAGATAGTTGTAGATATG 10634  
|||||

RESULT 13

US-09-342-353-1/c

; Sequence 1, Application US/09342353

; Patent No. 6248569

; GENERAL INFORMATION:

; APPLICANT: Dunn, John

; TITLE OF INVENTION: METHOD FOR INTRODUCING UNIDIRECTIONAL NESTED DELETIONS

; FILE REFERENCE: CIP OF U.S. Application 08/966,958

; CURRENT APPLICATION NUMBER: US/09/342,353

; CURRENT FILING DATE: 1999-06-29

; EARLIER APPLICATION NUMBER: 08/966,958

; EARLIER FILING DATE: 1997-11-10

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 10754

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-342-353-1

Query Match 0.3%; Score 83; DB 4; Length 10754;  
Best Local Similarity 100.0%; Pred. No. 3.5e-18;  
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|||||  
Db 10716 CAGCACCATTTAATAATAGGAATCCTTTCCCATTCGTTGTTTCTCAGGTTTGTC 10657  
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QY 29672 AGATCAGATAGTTGTAGATATG 29694  
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Db 10656 AGATCAGATAGTTGTAGATATG 10634  
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RESULT 14

US-08-687-080-68/c

; Sequence 68, Application US/08687080

; Patent No. 5968786

; GENERAL INFORMATION:

; APPLICANT: Gregory Dolganov

; TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof

; NUMBER OF SEQUENCES: 175

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dehlinger & Associates

; STREET: 350 Cambridge Avenue, Suite 250

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/687,080

; FILING DATE: 17-JUL-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/592,126

; FILING DATE: 26-JAN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Sholtz, Charles K.

; REGISTRATION NUMBER: 38,615

; REFERENCE/DOCKET NUMBER: 4600-0111.30

; TELEPHONE: (415) 324-0880

; TELEFAX: (415) 324-0960

; INFORMATION FOR SEQ ID NO: 68:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6623 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear





GenCore version 5.1.6  
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perfect score: 29921  
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Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1105431 seqs, 789497651 residues

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Maximum DB seq length:	2000000000
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3:	/cgn2_6/ptodata/2/pubpna	US06_NEW_PUB.seq.*	
4:	/cgn2_6/ptodata/2/pubpna	US06_PUBCOMB.seq.*	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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		Match					
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C 2	652	2.2		3718	9	US-10-258-557-3	Sequence 3, Appli
C 3	652	2.2		3736	9	US-10-258-557-1	Sequence 1, Appli
C 4	601	2.0		1934	9	US-10-086-623-5	Sequence 5, Appli
C 5	601	2.0		1934	9	US-10-060-539-5	Sequence 5, Appli
C 6	601	2.0		2253	9	US-10-086-623-7	Sequence 7, Appli
C 7	601	2.0		2253	9	US-10-260-539-7	Sequence 7, Appli
C 8	601	2.0		3798	10	US-09-915-582-17	Sequence 17, App
C 9	601	2.0		4001	10	US-09-915-582-35	Sequence 35, App
10	499	1.7		2726	10	US-09-915-582-37	Sequence 37, App
11	460	1.5		485	9	US-09-954-531-902	Sequence 902, App
C 12	377	1.3		1882	9	US-10-139-583-36	Sequence 36, Appl
C 13	377	1.3		1882	9	US-10-039-847A-1	Sequence 1, Appli
C 14	377	1.3		1882	9	US-10-226-559-1	Sequence 1, Appli
C 15	377	1.3		1882	9	US-10-274-638-1	Sequence 1, Appli
C 16	377	1.3		1882	10	US-09-808-372-1	Sequence 1, Appli
C 17	221	0.7		1162	9	US-10-028-072-185	Sequence 185, App
C 18	221	0.7		1162	9	US-10-121-049-185	Sequence 185, App
C 19	221	0.7		1162	9	US-10-123-904-185	Sequence 185, App

## ALIGNMENTS

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RESULT 1
US-10-083-853-1
; Sequence 1, Application US/10083853
; Patent NO US20020164709A1
; GENERAL INFORMATION:
; APPLICANT: Affimetrix, Inc
; APPLICANT: Shigetaka, Ron T
; APPLICANT: Siaghi-Rose, Michael A
; TITLE OF INVENTION: Nucleic Acid E
; FILE REFERENCE: 3385.1
; CURRENT APPLICATION NUMBER: US/10/
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US98/60/
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 29921
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-083-853-1

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Best Local Similarity	100.0%;	pred.	No. 0;			
Matches 29921;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;					
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DB	1	GTATATGTAAGAAAGCCCTCATCTTTTGATTTTTTAATATACAAGATGCTTTCTTTAAAGAGA	60			
QY	61	GCAAGATTCAAATTTGTTTGTGTTTCAAAATTTAAAAATAAATTTATCTCTCTAAATTTT	120			
DB	61	GCAAGATTCAAATTTGTTTGTGTTTCAAAATTTAAAAATAAATTTATCTCTCTAAATTTT	120			
QY	121	CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAGGATTTTAAAGAGTCT	180			
DB	121	CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAGGATTTTAAAGAGTCT	180			
QY	181	AACTCAACATATGTAAGCTCGGTGTACCTGGTTATATATACCAAAAAACATTTTGAT	240			
DB	181	AACTCAACATATGTAAGCTCGGTGTACCTGGTTATATATACCAAAAAACATTTTGAT	240			

QY	241	CTATATACATAGACATGAATATATTCTGTGTGTTTGTGCATATATAAACC	300
DB	241	CTATATACATAGACATGAATATATTCTGTGTGTTTGTGCATATATAAACC	300
QY	301	ACTATTATTAATCAATCCTATATTCTTAGGTATAGAAGTTGATGATATACCTTCTAC	360
DB	301	ACTATTATTAATCAATCCTATATTCTTAGGTATAGAAGTTGATGATATACCTTCTAC	360
QY	361	TTGCCATGGCATTAACAAGCAAGGCTGAGACTCAGCAACACCTTGTTGTTTCATTGCGATTG	420
DB	361	TTGCCATGGCATTAACAAGCAAGGCTGAGACTCAGCAACACCTTGTTGTTTCATTGCGATTG	420
QY	421	CAGCCTAGTAGTAAGTTTGGTTCGTGTAGAAAAGGTCCTTATCTCACCCCTCCTTAA	480
DB	421	CAGCCTAGTAGTAAGTTTGGTTCGTGTAGAAAAGGTCCTTATCTCACCCCTCCTTAA	480
QY	481	ACTAAAGGTTCTTTCAGGCTTAATGTAAGATGTGCACATCTCTTATCGAGGTGGTCTT	540
DB	481	ACTAAAGGTTCTTTCAGGCTTAATGTAAGATGTGCACATCTCTTATCGAGGTGGTCTT	540
QY	541	GAGCTGCAGATACAAATCACATCGTTGATGTGATCCAAGTGGATGTCAACTAGAGCCATG	600
DB	541	GAGCTGCAGATACAAATCACATCGTTGATGTGATCCAAGTGGATGTCAACTAGAGCCATG	600
QY	601	GTCTTAGCTCTACCCCTCCTTGTGATGTGCCAGGCTCAAACCTGTAATACCTAGGACAAG	660
DB	601	GTCTTAGCTCTACCCCTCCTTGTGATGTGCCAGGCTCAAACCTGTAATACCTAGGACAAG	660
QY	661	AAGCACATCTCCTGTTAGAAAGCCTTTGGAGTTCAACTAGTCAGATGCCACCTACTTAT	720
DB	661	AAGCACATCTCCTGTTAGAAAGCCTTTGGAGTTCAACTAGTCAGATGCCACCTACTTAT	720
QY	721	TACCTTTTGCACAACTAGTTCTTAGCCCTTTGAGACCCCAACAGACTATGGCTTGT	780
DB	721	TACCTTTTGCACAACTAGTTCTTAGCCCTTTGAGACCCCAACAGACTATGGCTTGT	780
QY	781	ATTAGAATGCACAGCTTGTCTATTAGAATGTACACATTTTTCAATAATTGACPTCCCTGAA	840
DB	781	ATTAGAATGCACAGCTTGTCTATTAGAATGTACACATTTTTCAATAATTGACPTCCCTGAA	840
QY	841	GTGAGGAATCAATGTATCCAGAGTAATGCCAGCATAACTTACCTGGAAGTACCAGAT	900
DB	841	GTGAGGAATCAATGTATCCAGAGTAATGCCAGCATAACTTACCTGGAAGTACCAGAT	900
QY	901	GATTTGATGTCTTACAGSTATTATTAAATAGCTTTCTAAGSGGCTGCTTTGGGCCAA	960
DB	901	GATTTGATGTCTTACAGSTATTATTAAATAGCTTTCTAAGSGGCTGCTTTGGGCCAA	960
QY	961	GTACTGTCCAAATATTATCGTAAAGATCCTCTGACCAAGGATGTGTTATAGATCAAT	1020
DB	961	GTACTGTCCAAATATTATCGTAAAGATCCTCTGACCAAGGATGTGTTATAGATCAAT	1020
QY	1021	ACAATCTTGAGCATATTATTAGATGGAGAGAAATGAATACAACCATGAATAAAAA	1080
DB	1021	ACAATCTTGAGCATATTATTAGATGGAGAGAAATGAATACAACCATGAATAAAAA	1080
QY	1081	TGCTGSPATATCAAAATCTTTGTTGAAGTAAACATGTTGCCCTGSAGTTGCTGSCAAG	1140
DB	1081	TGCTGSPATATCAAAATCTTTGTTGAAGTAAACATGTTGCCCTGSAGTTGCTGSCAAG	1140
QY	1141	ATGCCCGAAGCAGGAAGCTCTGGCTGCAAGTTCCCAGGCGAGATCAATCAGAAGCGGG	1200
DB	1141	ATGCCCGAAGCAGGAAGCTCTGGCTGCAAGTTCCCAGGCGAGATCAATCAGAAGCGGG	1200
QY	1201	TGATTTCTCCATTCOCAACTAGGATACCCAGTTTCATCTCAGTGGGACTGGTTAGACATTG	1260
DB	1201	TGATTTCTCCATTCOCAACTAGGATACCCAGTTTCATCTCAGTGGGACTGGTTAGACATTG	1260
QY	1261	GSTGCAGCCACGGAAGGTGAGCTGAAGCAGGTTGGGTGTCCTCAGCCGGAAGTGC	1320
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QY	1321	AAGGGGTGGGGATCTCTCTCCCCAGCCAAAGGAGCCATGAGAGACTGTACCAAGGAG	1380
DB	1321	AAGGGGTGGGGATCTCTCTCCCCAGCCAAAGGAGCCATGAGAGACTGTACCAAGGAG	1380
QY	1381	GAATGTTGACACTCTAGTCCAGATACTGCACTTTTCCCATAGTCTTTGCAACTGGCAGACC	1440
DB	1381	GAATGTTGACACTCTAGTCCAGATACTGCACTTTTCCCATAGTCTTTGCAACTGGCAGACC	1440
QY	1441	AGGAGATTTTCCCCAGTGTCTATGCCACCAGGGCCCTGGGTTTCAAGCACAAAACCTGGGC	1500
DB	1441	AGGAGATTTTCCCCAGTGTCTATGCCACCAGGGCCCTGGGTTTCAAGCACAAAACCTGGGC	1500
QY	1501	GGCCATTTGGACAGACACCGAGCTAGCCGACAGTATTATTTTTCATACCCAGTGGGC	1560
DB	1501	GGCCATTTGGACAGACACCGAGCTAGCCGACAGTATTATTTTTCATACCCAGTGGGC	1560
QY	1561	CTGGANTGCCACAGACAGAACCATTTCACTCAGGGATCCAAGTGGTCTCAGTGG	1620
DB	1561	CTGGANTGCCACAGACAGAACCATTTCACTCAGGGATCCAAGTGGTCTCAGTGG	1620
QY	1621	GTCCCAACCCCATGGAGCCAGCTAGCTAAGATCCAAGTGGCTTGAATTTCTCTGCCAGC	1680
DB	1621	GTCCCAACCCCATGGAGCCAGCTAGCTAAGATCCAAGTGGCTTGAATTTCTCTGCCAGC	1680
QY	1681	ACAGCAGTCTGAGATTTGACCTGGGATGTGTGAGTGGGAGGGGGCTCTGCCAT	1740
DB	1681	ACAGCAGTCTGAGATTTGACCTGGGATGTGTGAGTGGGAGGGGGCTCTGCCAT	1740
QY	1741	TGCTGAGGCTTGAGTAGGGAGGGGTTTTACCTCAAAAGTGTAAACAAGCTACTGGGA	1800
DB	1741	TGCTGAGGCTTGAGTAGGGAGGGGTTTTACCTCAAAAGTGTAAACAAGCTACTGGGA	1800
QY	1801	AGTTGAATGGGCGCCACCGCAGCTCAGCAAGCGCTGTGGCAAACTGCTCTCTAG	1860
DB	1801	AGTTGAATGGGCGCCACCGCAGCTCAGCAAGCGCTGTGGCAAACTGCTCTCTAG	1860
QY	1861	ATTCTCTCTTTTGGGCGAGTCTCTGAAAAGAAAGGAGCAGAGCCAGTCAAGGACTTT	1920
DB	1861	ATTCTCTCTTTTGGGCGAGTCTCTGAAAAGAAAGGAGCAGAGCCAGTCAAGGACTTT	1920
QY	1921	ATAGATATAAACCCCATCTCCCTGGGACAGAACTCTGGGGAAGGGGTGGTGGGTG	1980
DB	1921	ATAGATATAAACCCCATCTCCCTGGGACAGAACTCTGGGGAAGGGGTGGTGGGTG	1980
QY	1981	CAGCTTCTCAGACTTAAACATTTCCCTGGAGGCTCTGAAGAGAGCAGCGGATCTCCA	2040
DB	1981	CAGCTTCTCAGACTTAAACATTTCCCTGGAGGCTCTGAAGAGAGCAGCGGATCTCCA	2040
QY	2041	GCACAGCATTTGAGCTCTGATAAAGGACAGGCTGCTCTCAAGTGGGTCCCTGACCCCC	2100
DB	2041	GCACAGCATTTGAGCTCTGATAAAGGACAGGCTGCTCTCTCAAGTGGGTCCCTGACCCCC	2100
QY	2101	ATGTATCTGACTGGGAGACATCTCCCATTAGGGCCCAATAGACATTTTCATACAGGAGAC	2160
DB	2101	ATGTATCTGACTGGGAGACATCTCCCATTAGGGCCCAATAGACATTTTCATACAGGAGAC	2160
QY	2161	AGGGTCTGGAGTGGACCTCCAGCAACTCCAGCAGACCTGACAGAGAGGGGCTGACTGT	2220
DB	2161	AGGGTCTGGAGTGGACCTCCAGCAACTCCAGCAGACCTGACAGAGAGGGGCTGACTGT	2220
QY	2221	TAGAAGGAAAAAGTAAACAACAGAAAGGAATAGTATCAACATTTAAACAAAAGGACATCCAC	2280
DB	2221	TAGAAGGAAAAAGTAAACAACAGAAAGGAATAGTATCAACATTTAAACAAAAGGACATCCAC	2280
QY	2281	TCAGAGACCCCATCTGAGAGTCAACACATCAACAGCCAAAGGTAAATAAACACCAAAAAG	2340
DB	2281	TCAGAGACCCCATCTGAGAGTCAACACATCAACAGCCAAAGGTAAATAAACACCAAAAAG	2340
QY	2341	ATGGGAAAAACCCAGTGCAGAACCTGAAAAATTTCCAAAAACACAGAACTCTCTTCTCAAC	2400
DB	2341	ATGGGAAAAACCCAGTGCAGAACCTGAAAAATTTCCAAAAACACAGAACTCTCTTCTCAAC	2400
QY	2401	CAAGGATCACAACTCTCTCGCCAGCAAGGGGAACAAAACCCAGATGAGGAATGAGTTTGGG	2460

Db	2401	CAAAAGATCAAACTCTCCACGCAAGGGAACAAAACACAGATGGAGAATGAGTTTGAGG	2460
Qy	2461	AATTGACAGAAAGTAGGCTTCAGAAAGTGGGTAAATAACAAACTCTCCGAGCTAAAGAGC	2520
Db	2461	AATTGACAGAAAGTAGGCTTCAGAAAGTGGGTAAATAACAAACTCTCCGAGCTAAAGAGC	2520
Qy	2521	ATGTTCTAACCCCAATCAAGGAAGCTAAGAACCTTGAAAAAGGTTAGATGAATGCTAA	2580
Db	2521	ATGTTCTAACCCCAATCAAGGAAGCTAAGAACCTTGAAAAAGGTTAGATGAATGCTAA	2580
Qy	2581	CTAGAATAATCAGTGTAGAGAAAGACATAATGACCTGATGGAGCTGAAAAAGCAAGAC	2640
Db	2581	CTAGAATAATCAGTGTAGAGAAAGACATAATGACCTGATGGAGCTGAAAAAGCAAGAC	2640
Qy	2641	AAGAACTTCATGAAGCATACACAAAGCTTCAATAGCCAAATCGATCAAGCAGAGAAAGGA	2700
Db	2641	AAGAACTTCATGAAGCATACACAAAGCTTCAATAGCCAAATCGATCAAGCAGAGAAAGGA	2700
Qy	2701	TATCAGTGATGAAGATCAAAATTAATAAAGAAAGTGAGAGACAAAGATTACAGAAAAA	2760
Db	2701	TATCAGTGATGAAGATCAAAATTAATAAAGAAAGTGAGAGACAAAGATTACAGAAAAA	2760
Qy	2761	GAGTGAAGAAACACAAACAGCTTCAAGAAATATGGGACTATGTAAAAGACCAATC	2820
Db	2761	GAGTGAAGAAACACAAACAGCTTCAAGAAATATGGGACTATGTAAAAGACCAATC	2820
Qy	2821	TACATTTGATTTGGTGTCCCCAAAGTGTGGGAGAAATGAATCAAGTTGGAAGCACTC	2880
Db	2821	TACATTTGATTTGGTGTCCCCAAAGTGTGGGAGAAATGAATCAAGTTGGAAGCACTC	2880
Qy	2881	TTGAGGGTATATCCAGGAGAAATTTCCCATCTATCAGGCGAGCCCAACATTCAAATTCA	2940
Db	2881	TTGAGGGTATATCCAGGAGAAATTTCCCATCTATCAGGCGAGCCCAACATTCAAATTCA	2940
Qy	2941	GGAATATGAGAACACCAATTAAGATATCTCCTCGAGAGAACCAATTCGCAAGACACATAT	3000
Db	2941	GGAATATGAGAACACCAATTAAGATATCTCCTCGAGAGAACCAATTCGCAAGACACATAT	3000
Qy	3001	CTTCAGATTCACCAAGGTTGAAATGAAGAAAAAATGTTAAGGCGAGCAGAGAGAAGG	3060
Db	3001	CTTCAGATTCACCAAGGTTGAAATGAAGAAAAAATGTTAAGGCGAGCAGAGAGAAGG	3060
Qy	3061	TTGGGTTACCCCAAAAGGAGCCCAATCAGACATCAACAGCGGATCTCCCGGAGAAACCT	3120
Db	3061	TTGGGTTACCCCAAAAGGAGCCCAATCAGACATCAACAGCGGATCTCCCGGAGAAACCT	3120
Qy	3121	ACAGCCAGAGAGAGTGAGGCGCAATATTCACATCTTTAAGAAAAATATTTTCAACC	3180
Db	3121	ACAGCCAGAGAGAGTGAGGCGCAATATTCACATCTTTAAGAAAAATATTTTCAACC	3180
Qy	3181	CAGAAATTCATATCCAGCCAAACCAAGCTTCCCTAAGTGAAGGAGAAAAATAAATCCTCTAC	3240
Db	3181	CAGAAATTCATATCCAGCCAAACCAAGCTTCCCTAAGTGAAGGAGAAAAATAAATCCTCTAC	3240
Qy	3241	AGAGAAGCAATGCTGACAGATTTTGTACACCAAGCGCTGCTTCAAGAGAGCTCTGA	3300
Db	3241	AGAGAAGCAATGCTGACAGATTTTGTACACCAAGCGCTGCTTCAAGAGAGCTCTGA	3300
Qy	3301	AGGAAGCACCACATGGAAGGAGCAACTGGTACCCAGCCACTGCAAAAAACATCCCAATTT	3360
Db	3301	AGGAAGCACCACATGGAAGGAGCAACTGGTACCCAGCCACTGCAAAAAACATCCCAATTT	3360
Qy	3361	GTAAGACCAATGATGTATGAAGAAAGTGCATCACTAACGGGCAAAATAAACAGCTAG	3420
Db	3361	GTAAGACCAATGATGTATGAAGAAAGTGCATCACTAACGGGCAAAATAAACAGCTAG	3420
Qy	3421	TGTCATATGGCAGGATCAAAATTCACACATAATAATTAATTAACCTTAAATGGGCT	3480
Db	3421	TGTCATATGGCAGGATCAAAATTCACACATAATAATTAATTAACCTTAAATGGGCT	3480
Qy	3481	AAATTCCTCAATTAAGAGACACAGACTGGCAATTTGGATTAAGAGTCAAGACCCATCAGT	3540
Db	3481	AAATTCCTCAATTAAGAGACACAGACTGGCAATTTGGATTAAGAGTCAAGACCCATCAGT	3540
Qy	3541	GTGCTGTATTCAGGAGCCCATCTCACATGAAAAGACACATAGGCTCAAAATAAAGGG	3600
Db	3541	GTGCTGTATTCAGGAGCCCATCTCACATGAAAAGACACATAGGCTCAAAATAAAGGG	3600
Qy	3601	ATGAGGAGAGATTTACCAAGTAAATGTAAGAAAAACAAAAAGCAGGGGTGCAATCCT	3660
Db	3601	ATGAGGAGAGATTTACCAAGTAAATGTAAGAAAAACAAAAAGCAGGGGTGCAATCCT	3660
Qy	3661	AGTCTCTGATTAAGACAGACTTTAAACCAACAAAGATCAAAAGAGACAAAGAGCCCATTA	3720
Db	3661	AGTCTCTGATTAAGACAGACTTTAAACCAACAAAGATCAAAAGAGACAAAGAGCCCATTA	3720
Qy	3721	CATAATGCTTAAGAGCAATCAATGGAACAAAGAGCTAACTATCCTAAATATACATGCACC	3780
Db	3721	CATAATGCTTAAGAGCAATCAATGGAACAAAGAGCTAACTATCCTAAATATACATGCACC	3780
Qy	3781	CAATACAGGAGCAGCCAGATTCATAAAGCAAGTCTTTAGAGACCTACAAAGAGACTTTGA	3840
Db	3781	CAATACAGGAGCAGCCAGATTCATAAAGCAAGTCTTTAGAGACCTACAAAGAGACTTTGA	3840
Qy	3841	CTCCACACAAATATAGTGGAGTCTAAATAAATAATAGACACTTTAACACCCACCTGCC	3900
Db	3841	CTCCACACAAATATAGTGGAGTCTAAATAAATAATAGACACTTTAACACCCACCTGCC	3900
Qy	3901	AATATTAGGAGATCAATGAGACAGAAAAATTAACAAGGATATCCAGAGTTGAACTGAGC	3960
Db	3901	AATATTAGGAGATCAATGAGACAGAAAAATTAACAAGGATATCCAGAGTTGAACTGAGC	3960
Qy	3961	TCGAGCAACAGCGGACCTAATAGATATCTACAGAACTCCCCACCCCAAAATCAACAGATA	4020
Db	3961	TCGAGCAACAGCGGACCTAATAGATATCTACAGAACTCCCCACCCCAAAATCAACAGATA	4020
Qy	4021	TACACTCTCTCAGCATCATACACTATTTTAAATTTACACACTTAATTTTAACTAA	4080
Db	4021	TACACTCTCTCAGCATCATACACTATTTTAAATTTACACACTTAATTTTAACTAA	4080
Qy	4081	AACACTCTCAGCAAAATGCAAAAGACAGAAATCTTAAACAAACAGTCTCAGACTACAG	4140
Db	4081	AACACTCTCAGCAAAATGCAAAAGACAGAAATCTTAAACAAACAGTCTCAGACTACAG	4140
Qy	4141	TGCATCTATTAGAACTCAGAAATTAAGAACTCCTCAAAATCAACAACTACATGAGAA	4200
Db	4141	TGCATCTATTAGAACTCAGAAATTAAGAACTCCTCAAAATCAACAACTACATGAGAA	4200
Qy	4201	ACTGAACAACTGCTCTGATGACTACTGGTAAATAACAAATAAGAGGCAAAATAAA	4260
Db	4201	ACTGAACAACTGCTCTGATGACTACTGGTAAATAACAAATAAGAGGCAAAATAAA	4260
Qy	4261	GATGTTCTTTGAAACCAATGAGAACAAAGACACAATGTACAGAAATCTCTGGGCAATTT	4320
Db	4261	GATGTTCTTTGAAACCAATGAGAACAAAGACACAATGTACAGAAATCTCTGGGCAATTT	4320
Qy	4321	TAAAGCAGTGTAGAGGGAATTTATAGCACTAGATGCTTACAGAAAGCAAGCAAGAAAT	4380
Db	4321	TAAAGCAGTGTAGAGGGAATTTATAGCACTAGATGCTTACAGAAAGCAAGCAAGAAAT	4380
Qy	4381	ATCTTAAATAGACACTTTAATCACTACAAATTAAGAAAGTACAGAGAAAGCAACAAA	4440
Db	4381	ATCTTAAATAGACACTTTAATCACTACAAATTAAGAAAGTACAGAGAAAGCAACAAA	4440
Qy	4441	TTCAAAAGCTTAGCAGAGAAAGAAATTAACATGATCAGAGCAAGCACTGAAGGAGATAGA	4500
Db	4441	TTCAAAAGCTTAGCAGAGAAAGAAATTAACATGATCAGAGCAAGCACTGAAGGAGATAGA	4500
Qy	4501	GACACAAAAAGCCCTTCAAAATAATCAATGAATCCAGAGCTGGTTTTTTGAAAGATCA	4560
Db	4501	GACACAAAAAGCCCTTCAAAATAATCAATGAATCCAGAGCTGGTTTTTTGAAAGATCA	4560
Qy	4561	GCAAAATAGACCACTAGACAGACTTAATAAGAGAAAGAGAGAGAAATCAAGAGATGC	4620
Db	4561	GCAAAATAGACCACTAGACAGACTTAATAAGAGAAAGAGAGAGAAATCAAGAGATGC	4620



Db 6781 GACTTAATATATAGACATAAAACCATAAAAAACCAGAAAGAAAACCTTAGGCCAATACCATTTC 6840  
QY 6841 AGGATATGGACATGGCAAGAGCTTCATGACTAAAACACCAAAAGCAATGGCAACAAAAG 6900  
Db 6841 AGGATATGGACATGGCAAGAGCTTCATGACTAAAACACCAAAAGCAATGGCAACAAAAG 6900  
QY 6901 CCAAAATAGCAAGTGGGATCTGATTAACATATAGAGCTTCTGCACAGCAAAAAAAACT 6960  
Db 6901 CCAAAATAGCAAGTGGGATCTGATTAACATATAGAGCTTCTGCACAGCAAAAAAAACT 6960  
QY 6961 GTCATCAGAGTGAACAAGCAACCTACAGAATGGGAGAAAATTTTGGCAATCTATCGATCT 7020  
Db 6961 GTCATCAGAGTGAACAAGCAACCTACAGAATGGGAGAAAATTTTGGCAATCTATCGATCT 7020  
QY 7021 GACAAAGCTTAATATCCAGAGATCTACGAAGAACTTAAACAAATTTACAGAAAACAAAACA 7080  
Db 7021 GACAAAGCTTAATATCCAGAGATCTACGAAGAACTTAAACAAATTTACAGAAAACAAAACA 7080  
QY 7081 ACCCGGTCAAAATATGGCAAGGATATGACGACAGACCTTCTCAAAAAGAGACATTTATG 7140  
Db 7081 ACCCGGTCAAAATATGGCAAGGATATGACGACAGACCTTCTCAAAAAGAGACATTTATG 7140  
QY 7141 CAGCAACAAATATGAAAAAAACCTCATCATCTGCTGTAGAGAAAATGCAAAAACA 7200  
Db 7141 CAGCAACAAATATGAAAAAAACCTCATCATCTGCTGTAGAGAAAATGCAAAAACA 7200  
QY 7201 AAACACAGTGCATACCATCTCATGCTAGTGTAGAACTTACACTAAAAGTCAGGAA 7260  
Db 7201 AAACACAGTGCATACCATCTCATGCTAGTGTAGAACTTACACTAAAAGTCAGGAA 7260  
QY 7261 ACACAAATGCTGGAGAGATGTGGAGAAATAGGAACACTTTTCCACTGTTGGTGGGAAT 7320  
Db 7261 ACACAAATGCTGGAGAGATGTGGAGAAATAGGAACACTTTTCCACTGTTGGTGGGAAT 7320  
QY 7321 GTAATATAGTTCACCAATGTGGAGAGAGTGTGGAGAAATAGGAACACTTTTCCACTGTTGGTGGGAAT 7380  
Db 7321 GTAATATAGTTCACCAATGTGGAGAGAGTGTGGAGAAATAGGAACACTTTTCCACTGTTGGTGGGAAT 7380  
QY 7381 AAATATCATTTGACCCAGCAATCCCATTTACTGAGTATATACCAAGAAATATTAATCAT 7440  
Db 7381 AAATATCATTTGACCCAGCAATCCCATTTACTGAGTATATACCAAGAAATATTAATCAT 7440  
QY 7441 TCTATATTAAGACACATGCACATATGTTTATTTAGCAGCTATGATCAACAATAGCAAGA 7500  
Db 7441 TCTATATTAAGACACATGCACATATGTTTATTTAGCAGCTATGATCAACAATAGCAAGA 7500  
QY 7501 CTTGGAACCAACCCAAATGTCATCAGTATAGACTGGATGAAGAAAACATGGCACATAT 7560  
Db 7501 CTTGGAACCAACCCAAATGTCATCAGTATAGACTGGATGAAGAAAACATGGCACATAT 7560  
QY 7561 ACACCATGAATATCTATGACGCCATATAAGAGATGAGTTCATGCTCTTGCAGAGATATG 7620  
Db 7561 ACACCATGAATATCTATGACGCCATATAAGAGATGAGTTCATGCTCTTGCAGAGATATG 7620  
QY 7621 GATGAAGCTGGAACCAATCTCAGCAAACTTACACAGAAAGCAAGAAAACCAACACCA 7680  
Db 7621 GATGAAGCTGGAACCAATCTCAGCAAACTTACACAGAAAGCAAGAAAACCAACACCA 7680  
QY 7681 CATGTTCTCACTTGTAGTGGAGTTGAACATGAGAGAGATGGACACAGGGAGGAA 7740  
Db 7681 CATGTTCTCACTTGTAGTGGAGTTGAACATGAGAGAGATGGACACAGGGAGGAA 7740  
QY 7741 CATCACACACAGGTCTGTTGTTGGTGCAGGACTAGGGAAGGATAGCATTTAGGAGAA 7800  
Db 7741 CATCACACACAGGTCTGTTGTTGGTGCAGGACTAGGGAAGGATAGCATTTAGGAGAA 7800  
QY 7801 ATACCTAATGTAGATGACGGTTGATGGTGCAGCAAGCCACCATGGCACATGTATACCT 7860  
Db 7801 ATACCTAATGTAGATGACGGTTGATGGTGCAGCAAGCCACCATGGCACATGTATACCT 7860  
QY 7861 ATGTAAACAAACCTGCACATCTGCACATGTATACCCCAACACTTAAAGTATTTAAAAAATA 7920  
Db 7861 ATGTAAACAAACCTGCACATCTGCACATGTATACCCCAACACTTAAAGTATTTAAAAAATA 7920

QY 7921 CACAAACATGTTGCCCTGATGAAGGTCATTAGTGGCCATAAATAAGTAAATGTGTTTT 7980  
Db 7921 CACAAACATGTTGCCCTGATGAAGGTCATTAGTGGCCATAAATAAGTAAATGTGTTTT 7980  
QY 7981 ATGTTTTTATATATTTGTTAAACATATATATCTTTTACCATTTTAAACAAATCAGGTTCC 8040  
Db 7981 ATGTTTTTATATATTTGTTAAACATATATATCTTTTACCATTTTAAACAAATCAGGTTCC 8040  
QY 8041 ACTAAATCTTTGTATATTAATACCTGTGTATCAATACAGCATTTCTTAAATCAATAAGT 8100  
Db 8041 ACTAAATCTTTGTATATTAATACCTGTGTATCAATACAGCATTTCTTAAATCAATAAGT 8100  
QY 8101 ATATCATTTAATTTTAAATTCATAGTTTAAACATAAATTTCTTAAATTAGTAGTAAATA 8160  
Db 8101 ATATCATTTAATTTTAAATTCATAGTTTAAACATAAATTTCTTAAATTAGTAGTAAATA 8160  
QY 8161 GAAGCAACCTCTCTCCCTGCAGTGGCTTCATTTAGTGAATATTTAGCTATTACATAG 8220  
Db 8161 GAAGCAACCTCTCTCCCTGCAGTGGCTTCATTTAGTGAATATTTAGCTATTACATAG 8220  
QY 8221 ACATATACCTTGGTAAAATTTCCATCTTCTTTTCTAAATATACATAGTCAGATTAATATAT 8280  
Db 8221 ACATATACCTTGGTAAAATTTCCATCTTCTTTTCTAAATATACATAGTCAGATTAATATAT 8280  
QY 8281 ATTTACTTTTATGTTCTTAGATCCCGGTAGCTTTTATTTTGTATTTTCTCCCATTTTCT 8340  
Db 8281 ATTTACTTTTATGTTCTTAGATCCCGGTAGCTTTTATTTTGTATTTTCTCCCATTTTCT 8340  
QY 8341 TTTAGATTTCTAAACTTTGGTCATGGCACCATTAAACAATTTCTATAGCATTTTACAGTTTTT 8400  
Db 8341 TTTAGATTTCTAAACTTTGGTCATGGCACCATTAAACAATTTCTATAGCATTTTACAGTTTTT 8400  
QY 8401 GAATAAATTTGCACAGGCACATATTTTCTTTTCTTTTACCCTCAGACAAATCTTTCACA 8460  
Db 8401 GAATAAATTTGCACAGGCACATATTTTCTTTTCTTTTACCCTCAGACAAATCTTTCACA 8460  
QY 8461 TGGTGGAAAAGGTATCATTTATGCCACCTTTATCTGAGATTTCTAAAGAGGATTAAGTACC 8520  
Db 8461 TGGTGGAAAAGGTATCATTTATGCCACCTTTATCTGAGATTTCTAAAGAGGATTAAGTACC 8520  
QY 8521 TTGTCAGGGTCTTCCCTGACTTGGACCTGGGACCGAGACCTGGGATCAGACATTTAA 8580  
Db 8521 TTGTCAGGGTCTTCCCTGACTTGGACCTGGGACCGAGACCTGGGATCAGACATTTAA 8580  
QY 8581 GCTCCTAGCATATCTGACTTTGAGCCCTCTTAACATGCCCTCAATTTCTTTTATGTCT 8640  
Db 8581 GCTCCTAGCATATCTGACTTTGAGCCCTCTCTAACATGCCCTCAATTTCTTTTATGTCT 8640  
QY 8641 CAAGGGTGTGCTGGCTCCCATGTGAACCCGCGAGGAGACCTGTGATGCTTTGCTGAA 8700  
Db 8641 CAAGGGTGTGCTGGCTCCCATGTGAACCCGCGAGGAGACCTGTGATGCTTTGCTGAA 8700  
QY 8701 CTTTTGCTTAGTGAAGTTAGATGCTGAGTCCCTGCACTATGCATCAGGTCG 8760  
Db 8701 CTTTTGCTTAGTGAAGTTAGATGCTGAGTCCCTGCACTATGCATCAGGTCG 8760  
QY 8761 CACATTCCTTTTATTTAGAAATTTTGGCAATGTTTCCATAGACGGTCCAGTGAGCAGGG 8820  
Db 8761 CACATTCCTTTTATTTAGAAATTTTGGCAATGTTTCCATAGACGGTCCAGTGAGCAGGG 8820  
QY 8821 AATAAATCAGTGCATTTGTTTAAATGTTCAATCAAGTTAGGGCACTCTCTGATGCAGAT 8880  
Db 8821 AATAAATCAGTGCATTTGTTTAAATGTTCAATCAAGTTAGGGCACTCTCTGATGCAGAT 8880  
QY 8881 GGAAGATGGAGATCTGTTTGTAGAAAACCTTCAAAAGACTTGTCTGATGCAAGTTGGCAG 8940  
Db 8881 GGAAGATGGAGATCTGTTTGTAGAAAACCTTCAAAAGACTTGTCTGATGCAAGTTGGCAG 8940  
QY 8941 GGGTGGAGGAGGAATAACCTTAAGAAAGTTCTTTAGGAGACAAAGTGTCTGAGAAATTTT 9000  
Db 8941 GGGTGGAGGAGGAATAACCTTAAGAAAGTTCTTTAGGAGACAAAGTGTCTGAGAAATTTT 9000





Dd	11161	TTAAATGATTTTGACAGACCTTTAGAGGATTTATGACTACATGTTGAGCCTACCAATTGC	11220
Qy	11221	AGAAAACATAATGAAAGCCTGGTGGGCACTACATTTACAGACATGGCATTAGCATGG	11280
Dd	11221	AGAAAACATAATGAAAGCCTGGTGGGCACTACATTTACAGACATGGCATTAGCATGG	11280
Qy	11281	GTATCACTCATGACACAGATGGGCCCTGCTGCTGGGGAGTACCTTTGCCCCATGTGGCA	11340
Dd	11281	GTATCACTCATGACACAGATGGGCCCTGCTGCTGGGGAGTACCTTTGCCCCATGTGGCA	11340
Qy	11341	AGTTTCCGCTTTGGCAGGAAGCCCTGATGTGAAGCTAGATTGAGAAGGGAGAGGTGG	11400
Dd	11341	AGTTTCCGCTTTGGCAGGAAGCCCTGATGTGAAGCTAGATTGAGAAGGGAGAGGTGG	11400
Qy	11401	CAGTTTGTATACCTTAAACAAGAGTTCACTAACTTGTAACTGAGTCACTCAGGCAAGAA	11460
Dd	11401	CAGTTTGTATACCTTAAACAAGAGTTCACTAACTTGTAACTGAGTCACTCAGGCAAGAA	11460
Qy	11461	TGTAATCAGAACTGAGAAAGCCAGACAGGCTCTCATCTAACTTCCACCCACATCTGCTTT	11520
Dd	11461	TGTAATCAGAACTGAGAAAGCCAGACAGGCTCTCATCTAACTTCCACCCACATCTGCTTT	11520
Qy	11521	GTACTTTATAGTCTTCAGATGCCCTTCATTCACCCAGTATCCCCAGGTGGTAAGAAGACA	11580
Dd	11521	GTACTTTATAGTCTTCAGATGCCCTTCATTCACCCAGTATCCCCAGGTGGTAAGAAGACA	11580
Qy	11581	TGTGTTATCATTCGCCATTTGTCAGATGAGTGAATTAACCTTTTATAAGCAGTCTATAA	11640
Dd	11581	TGTGTTATCATTCGCCATTTGTCAGATGAGTGAATTAACCTTTTATAAGCAGTCTATAA	11640
Qy	11641	CATTACTGTCTGATCATATCTTTATCTTTTTCATTTTACCTAGCATTTTCAACCCACC	11700
Dd	11641	CATTACTGTCTGATCATATCTTTATCTTTTTCATTTTACCTAGCATTTTCAACCCACC	11700
Qy	11701	AATTTGTTTTATCTTACACAAATTCATTAGATTTTGGGGCAGGATTAAGTGTAC	11760
Dd	11701	AATTTGTTTTATCTTACACAAATTCATTAGATTTTGGGGCAGGATTAAGTGTAC	11760
Qy	11761	AACAGATATGAATGATGATTAATTCAGGTTTGCCTGGGAACCTCAAAATTTGAGGTAT	11820
Dd	11761	AACAGATATGAATGATGATTAATTCAGGTTTGCCTGGGAACCTCAAAATTTGAGGTAT	11820
Qy	11821	TATGGGGATTAAGTAGGAACCTGAGGCCCTGGGAAGTTTAAAGTGGCTGGTCCACGT	11880
Dd	11821	TATGGGGATTAAGTAGGAACCTGAGGCCCTGGGAAGTTTAAAGTGGCTGGTCCACGT	11880
Qy	11881	TGCCCCCTCCATGTGGCAAGCTGGAACCCAGACCCACATCTTTCTAGTCCCTCAAGTTT	11940
Dd	11881	TGCCCCCTCCATGTGGCAAGCTGGAACCCAGACCCACATCTTTCTAGTCCCTCAAGTTT	11940
Qy	11941	TCCTCTCTATTTGCCCTCTCTTGTAGGAAACATCACAGACCATGAGGCTTCACTTAAAG	12000
Dd	11941	TCCTCTCTATTTGCCCTCTCTTGTAGGAAACATCACAGACCATGAGGCTTCACTTAAAG	12000
Qy	12001	GTGGAGAAAGGACAAGAGGAGAGACTCCACAAGTTCTAGCTATGAGGTTTCCAAAAA	12060
Dd	12001	GTGGAGAAAGGACAAGAGGAGAGACTCCACAAGTTCTAGCTATGAGGTTTCCAAAAA	12060
Qy	12061	AATAACAGAAAGAGATTTCTTGACTTTTATGTTAGGTATTAATCATGACCCAAAA	12120
Dd	12061	AATAACAGAAAGAGATTTCTTGACTTTTATGTTAGGTATTAATCATGACCCAAAA	12120
Qy	12121	ACFCCCTCCCTATGCTAGAGAAGAAACTCCTCGCGGAAATTTATTTCTGTTTCTT	12180
Dd	12121	ACTCCCTCCCTATGCTAGAGAAGAAACTCCTCGCGGAAATTTATTTCTGTTTCTT	12180
Qy	12181	TGCTCTCAATTTGAAATTTAGTACTTTTTTTTCAATAACAGACGTTTCAACATGTAA	12240
Dd	12181	TGCTCTCAATTTGAAATTTAGTACTTTTTTTTCAATAACAGACGTTTCAACATGTAA	12240
Qy	12241	AAACAAGTACTATTTCTTTTACCTCAAACTGAGGTCAACAGTGTATTACTTACCTC	12300
Dd	12241	AAACAAGTACTATTTCTTTTACCTCAAACTGAGGTCAACAGTGTATTACTTACCTC	12300

QY	13381	CTTTTGTGTTGAGATGTGGTCTTACTCTGTCAACCAGGCTAGAGTGCAGTTGCTATGATC	13440		Db	14461	ACTAGGCTCAAGCAACCCCACTTCTGGAAATGGAATAAGCTTTTGTGTTTCCACAG	14520	
Db	13381	CTTTTGTGTTGAGATGTGGTCTTACTCTGTCAACCAGGCTAGAGTGCAGTTGCTATGATC	13440		QY	14521	GGCACTTGACAGTGATAATTTGTGACACATCTCAAGGTTATTTTCAGAGTCTCAGGGGCAT	14580	
QY	13441	ATGTTCTGTCGCAACCTTGAACCTCTGGGCTCAAGCAATCTCCTGCCCTCAGCCTCCCAA	13500		Db	14521	GGCACTTGACAGTGATAATTTGTGACACATCTCAAGGTTATTTTCAGAGTCTCAGGGGCAT	14580	
Db	13441	ATGTTCTGTCGCAACCTTGAACCTCTGGGCTCAAGCAATCTCCTGCCCTCAGCCTCCCAA	13500		QY	14581	ATGACAGGAGTGTGTTTCCAGGTAAGCAGTTACTGGCTGGTGATGGATGTTATTTTC	14640	
QY	13501	GTAGCTCAGACACACAGACATCTCCACATTTGGCTACTTAAATAAATTCCTTTT	13560		Db	14581	ATGACAGGAGTGTGTTTCCAGGTAAGCAGTTACTGGCTGGTGATGGATGTTATTTTC	14640	
Db	13501	GTAGCTCAGACACACAGACATCTCCACATTTGGCTACTTAAATAAATTCCTTTT	13560		QY	14641	CTTTCATCCAGCACTTGACAGAGTGATTTATAGAGCTTTTGACAGTCTTAGAAGTAA	14700	
QY	13561	TATTAATTAATTTTATTTTATAGAGATGGGGGCTCTCGCTATGTTGACCCGGTTGAT	13620		Db	14641	CTTTCATCCAGCACTTGACAGAGTGATTTATAGAGCTTTTGACAGTCTTAGAAGTAA	14700	
Db	13561	TATTAATTAATTTTATTTTATAGAGATGGGGGCTCTCGCTATGTTGACCCGGTTGAT	13620		QY	14701	ATATTAGGACACATGCTTTAAAGAGATGCTTTAGATACAGTTTCAAGGATGCCAATGTT	14760	
QY	13621	CTTGAACCTATAGCCTCAAGGATCATCCACCTTGGCCTCTCAAGTCTGAGATTACA	13680		Db	14701	ATATTAGGACACATGCTTTAAAGAGATGCTTTAGATACAGTTTCAAGGATGCCAATGTT	14760	
Db	13621	CTTGAACCTATAGCCTCAAGGATCATCCACCTTGGCCTCTCAAGTCTGAGATTACA	13680		QY	14761	TCAAATCCACTCATCGCACTGAACAAAGAGATCAAGAGTTTCCCTCTACACATTAAC	14820	
QY	13681	GGCATGAGCCACTGCTCTGGCTAAGAAATCCTTATCTCAAGACAAAGGTAGAACAA	13740		Db	14761	TCAAATCCACTCATCGCACTGAACAAAGAGATCAAGAGTTTCCCTCTACACATTAAC	14820	
Db	13681	GGCATGAGCCACTGCTCTGGCTAAGAAATCCTTATCTCAAGACAAAGGTAGAACAA	13740		QY	14821	GAGACAGAAATTTGCAAGTAATGTTATGTTAGAGAGATAAGAAAGAACTAAGAGG	14880	
QY	13741	TAGAATCTGAACAAACAGCCCTTGCTAATTTTCCCGCTTTATTAACATTAAGATCAT	13800		Db	14821	GAGACAGAAATTTGCAAGTAATGTTATGTTAGAGAGATAAGAAAGAACTAAGAGG	14880	
Db	13741	TAGAATCTGAACAAACAGCCCTTGCTAATTTTCCCGCTTTATTAACATTAAGATCAT	13800		QY	14881	AGGAGGTAAGCCAGCCCTTCAGTGTCTTCAAACTAAGTAAATTTTAAATCAAGCTAA	15000	
QY	13801	TCGCGCCTATCATATTTCTCCACACTATCCACACTTTATCAAACTTACTGTAA	13860		Db	14881	AGGAGGTAAGCCAGCCCTTCAGTGTCTTCAAACTAAGTAAATTTTAAATCAAGCTAA	15000	
Db	13801	TCGCGCCTATCATATTTCTCCACACTATCCACACTTTATCAAACTTACTGTAA	13860		QY	14941	TGGGGTCTATGTTTCACTCTCTCTCCCAATAAGTAAATTTTAAATCAAGCTAA	15000	
QY	13861	ATCAGGTTGAACCACTTTTGGGCTCTCTTACCAAGGCTCTGTGTCACCTGTAACAT	13920		Db	14941	TGGGGTCTATGTTTCACTCTCTCTCCCAATAAGTAAATTTTAAATCAAGCTAA	15000	
Db	13861	ATCAGGTTGAACCACTTTTGGGCTCTCTTACCAAGGCTCTGTGTCACCTGTAACAT	13920		QY	15001	AATTTCTATCTGAGCATAGAGTCAAGATAAAATAAAGCACTCCCAATAATACATCAA	15060	
QY	13921	ATTCATAAATGAGTACACTTTTCCTTTGTTATTCGTCTTTGTTATAGTGGCCTCAG	13980		Db	15001	AATTTCTATCTGAGCATAGAGTCAAGATAAAATAAAGCACTCCCAATAATACATCAA	15060	
Db	13921	ATTCATAAATGAGTACACTTTTCCTTTGTTATTCGTCTTTGTTATAGTGGCCTCAG	13980		QY	15061	CTGACCTTGAATGTTCTTCTCCTCAGAGTTACTACTAGGTAGAGACCTTGTCATCT	15120	
QY	13981	CATGACCTTAGGAGGCTGGAAGAAAGGTATTTTCCCTACTCTATATCTAGTATATCC	14040		Db	15061	CTGACCTTGAATGTTCTTCTCCTCAGAGTTACTACTAGGTAGAGACCTTGTCATCT	15120	
Db	13981	CATGACCTTAGGAGGCTGGAAGAAAGGTATTTTCCCTACTCTATATCTAGTATATCC	14040		QY	15121	TTATTTTAACTATAACCTGATTACTGCAATTCGCAATTTATCTTGGGTTATGTTAAAG	15180	
QY	14041	AAGAAGCATAGATGATTTTGAAGAGAGGAAATACTTCAACAGGCTACTTCAAAAC	14100		Db	15121	TTATTTTAACTATAACCTGATTGCAATTCGCAATTTATCTTGGGTTATGTTAAAG	15180	
Db	14041	AAGAAGCATAGATGATTTTGAAGAGAGGAAATACTTCAACAGGCTACTTCAAAAC	14100		QY	15181	TTATAAAATTCAGGTTCTTAGAAGTGAAGGCAACATCCAATCTAGAGTTCACTAGTCA	15240	
QY	14101	TTTTGAGACGAAGAAATAAAGACAGTCAATTTTACTGCACAGTGAACCCGCTCAA	14160		Db	15181	TTATAAAATTCAGGTTCTTAGAAGTGAAGGCAACATCCAATCTAGAGTTCACTAGTCA	15240	
Db	14101	TTTTGAGACGAAGAAATAAAGACAGTCAATTTTACTGCACAGTGAACCCGCTCAA	14160		QY	15241	TACAAATAAACAACATGAACATAGATGATAGATCTCTAGATATCAGAACATTTTT	15300	
QY	14161	AACTTACAGGACAACTAATATGACCTGTGAAGAAAGCAATATTAGCTTCGTTAGAAG	14220		Db	15241	TACAAATAAACAACATGAACATAGATGATAGATCTCTAGATATCAGAACATTTTT	15300	
Db	14161	AACTTACAGGACAACTAATATGACCTGTGAAGAAAGCAATATTAGCTTCGTTAGAAG	14220		QY	15301	TTTCTCTTGAACACAGTGGGTTGATCAAGCAATTTCTTATGACTTAAAGAAAATATGTTCC	15360	
QY	14221	TTCCAGTTTCCAGATTTAAATTCCTTAAGTTTGAAGCTGAAATATTTTGTGGAGATCA	14280		Db	15301	TTTCTCTTGAACACAGTGGGTTGATCAAGCAATTTCTTATGACTTAAAGAAAATATGTTCC	15360	
Db	14221	TTCCAGTTTCCAGATTTAAATTCCTTAAGTTTGAAGCTGAAATATTTTGTGGAGATCA	14280		QY	15361	ATGTAGGGTAAATAGTGTTCCTGCTGCTGAAGTAAAGTATGCTCATGTTGGAACATTTT	15420	
QY	14281	CACAGCCTGTTATGTGACAAGGTCTCATACCCCTTAAAGGCTGCTCATCTTTCACAGA	14340		Db	15361	ATGTAGGGTAAATAGTGTTCCTGCTGCTGAAGTAAAGTATGCTCATGTTGGAACATTTT	15420	
Db	14281	CACAGCCTGTTATGTGACAAGGTCTCATACCCCTTAAAGGCTGCTCATCTTTCACAGA	14340		QY	15421	CCTACATTTTCCCAAGTGAATAATATCAATTTTACATCTCAATTTTGGTTAATCCAGAA	15480	
QY	14341	AACTCATTTACATCTCATCAGTTGCAACCTAGCTGGGAACTGGTTTCTCATTTCT	14400		Db	15421	CCTACATTTTCCCAAGTGAATAATATCAATTTTACATCTCAATTTTGGTTAATCCAGAA	15480	
Db	14341	AACTCATTTACATCTCATCAGTTGCAACCTAGCTGGGAACTGGTTTCTCATTTCT	14400		QY	15481	GTTACTCTCTACTACTACGATTTTGTGTTGTTTTCAGAAATAGAAATCAAAACCAAA	15540	
QY	14401	CAGAGTAAAGATACAGACACAGAAATTCAGAAATAAAGGACTAGAAATTTTCCCTAATG	14460		Db	15481	GTTACTCTCTACTACTACGATTTTGTGTTGTTTTCAGAAATAGAAATCAAAACCAAA	15540	
Db	14401	CAGAGTAAAGATACAGACACAGAAATTCAGAAATAAAGGACTAGAAATTTTCCCTAATG	14460		QY	15541	CACCACACCACCAAAAGGCTTCCAAAAACAGTTTACAAAGCTGGAGATTTTGTGTTA	15600	
QY	14461	ACTAGGCTCAAGCAACCCCACTTCTGGAAATGGAATAAGCCTTTTGTGTTTCCACAG	14520						

Db	15541	CACCACCAACACAAAAGCCCTCCAAAACAGTTTTTAAAGCTGGAGATTTTCTTTA	15600
QY	15601	GAGAGAACTACCTATTCCCTTGTGTGGTGACACCTTTTAAAAATATTATTATATACTTT	15660
Db	15601	GAGAGAACTACCTATTCCCTTGTGTGGTGACACCTTTTAAAAATATTATTATATACTTT	15660
QY	15661	AAGTTGTGGATACTTGTGCAGAACGTGCAGGTTTCTTACGTAGGTATACACGTGCCATG	15720
Db	15661	AAGTTGTGGATACTTGTGCAGAACGTGCAGGTTTCTTACGTAGGTATACACGTGCCATG	15720
QY	15721	GTGGTTGTGTCACCCCTTTAAACCCATCACTACATTTAGTATTTCCTTAAAGCTATACC	15780
Db	15721	GTGGTTGTGTCACCCCTTTAAACCCATCACTACATTTAGTATTTCCTTAAAGCTATACC	15780
QY	15781	TCCCCAAACCCCAACCCAGCAGCCCGGCTGTGATGTCCTTCCCTGTGTGCC	15840
Db	15781	TCCCCAAACCCCAACCCAGCAGCCCGGCTGTGATGTCCTTCCCTGTGTGCC	15840
QY	15841	TGTGTTCACTCTCACTTATGAGTGAGAACATGTGTGGTGGTGTGTTTCTTCCCTGTGT	15900
Db	15841	TGTGTTCACTCTCACTTATGAGTGAGAACATGTGTGGTGGTGTGTTTCTTCCCTGTGT	15900
QY	15901	AGTTTCTGAGATGATGTTCTAGCTTCATCCGCTCTCTGCAAGGACGTGAACCTCA	15960
Db	15901	AGTTTCTGAGATGATGTTCTAGCTTCATCCGCTCTCTGCAAGGACGTGAACCTCA	15960
QY	15961	TCCTTTTTAAGGCTCAAAAGTATCCATGGTGTATATGTGCACATTTCTTTATCCAG	16020
Db	15961	TCCTTTTTAAGGCTCAAAAGTATCCATGGTGTATATGTGCACATTTCTTTATCCAG	16020
QY	16021	TCATCACTGATGGGATTTGGTGTGTTCCAAAGTCTTTGCTATTTGTAATAGTGTGCA	16080
Db	16021	TCATCACTGATGGGATTTGGTGTGTTCCAAAGTCTTTGCTATTTGTAATAGTGTGCA	16080
QY	16081	ATAACATATGTGTGATGCTCTTTATAGCAGAATGATCTATAATCATTTGTTATATAC	16140
Db	16081	ATAACATATGTGTGATGCTCTTTATAGCAGAATGATCTATAATCATTTGTTATATAC	16140
QY	16141	CCAGTAATGGGATTTGTGTGGACACTGTAGGAGAGCAACTCAAAACAGTAATTCCTAACAA	16200
Db	16141	CCAGTAATGGGATTTGTGTGGACACTGTAGGAGAGCAACTCAAAACAGTAATTCCTAACAA	16200
QY	16201	TGATGTTTGTTCATATTTAGTTTATATTTTAAACATATTTCTGCATGATGTTTAAACA	16260
Db	16201	TGATGTTTGTTCATATTTAGTTTATATTTTAAACATATTTCTGCATGATGTTTAAACA	16260
QY	16261	TCTTGCAAAATATATTTTATATGATGCTATTTTATTTGACCCCTCAGAGCAACTCTGGAAG	16320
Db	16261	TCTTGCAAAATATATTTTATATGATGCTATTTTATTTGACCCCTCAGAGCAACTCTGGAAG	16320
QY	16321	GGTTATCTGATATATTTTTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG	16380
Db	16321	GGTTATCTGATATATTTTTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG	16380
QY	16381	TTAGTCACTTGCATGTTTCCACAATATAAAGTAATTTAGAGCTGCTGCTGCTGCTGCTG	16440
Db	16381	TTAGTCACTTGCATGTTTCCACAATATAAAGTAATTTAGAGCTGCTGCTGCTGCTGCTG	16440
QY	16441	GAAGAGCTCTAACTG	16500
Db	16441	GAAGAGCTCTAACTG	16500
QY	16501	TGTATATATATATATATATACACACACACACACACATATATATATATATATATA	16560
Db	16501	TGTATATATATATATATATACACACACACACACACACATATATATATATATATA	16560
QY	16561	TGTAATTTTTTTTTCAGATGAGTTTCTTTTACCAGGCTGGAGTGCATGCGCGATC	16620
Db	16561	TGTAATTTTTTTTTCAGATGAGTTTCTTTTACCAGGCTGGAGTGCATGCGCGATC	16620
QY	16621	TCAGCTCACTGCAACCTCCGCTCCGCGGTTCAAGTGATTTCTCCGCTCAGCTCCTGA	16680
Db	16621	TCAGCTCACTGCAACCTCCGCTCCGCGGTTCAAGTGATTTCTCCGCTCAGCTCCTGA	16680
QY	16681	GTAGCTGGGATTACAGGTGCCCTCAGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	16740
Db	16681	GTAGCTGGGATTACAGGTGCCCTCAGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	16740
QY	16741	ACGGGTTTTTGGCATGTTGGCCACGCTGTTTGAACCTCCTGACCTCAGGTGATCCACCC	16800
Db	16741	ACGGGTTTTTGGCATGTTGGCCACGCTGTTTGAACCTCCTGACCTCAGGTGATCCACCC	16800
QY	16801	ACCTCGGCTCCCAAAAGTCTAGGATTACAGGCTGAGCACTGCGCCCGGCTATCTTT	16860
Db	16801	ACCTCGGCTCCCAAAAGTCTAGGATTACAGGCTGAGCACTGCGCCCGGCTATCTTT	16860
QY	16861	TATGCTCAATAAAGTCTATATATTACTAGTGTATAAGAAAACCATAGACCTCGGAACCA	16920
Db	16861	TATGCTCAATAAAGTCTATATATTACTAGTGTATAAGAAAACCATAGACCTCGGAACCA	16920
QY	16921	GTGGATTGAGTTGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	16980
Db	16921	GTGGATTGAGTTGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	16980
QY	16981	ACTGATCCTCTTAGGCTCAGTTTACTCACCTATAAAAAAGAAATAAATACTGACATT	17040
Db	16981	ACTGATCCTCTTAGGCTCAGTTTACTCACCTATAAAAAAGAAATAAATACTGACATT	17040
QY	17041	TTTACAATATTTGTGATGGGCTGAATGAGCTAATGATTTACTTACAATAGTTTTTGTGTC	17100
Db	17041	TTTACAATATTTGTGATGGGCTGAATGAGCTAATGATTTACTTACAATAGTTTTTGTGTC	17100
QY	17101	AAGCAATAATGCGCATTTGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAG	17160
Db	17101	AAGCAATAATGCGCATTTGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAG	17160
QY	17161	TCCTATATCTTTTACTTTTGTCTATTTTGGCAATATCCAAAGAGCTGATTCCTGAGTAG	17220
Db	17161	TCCTATATCTTTTACTTTTGTCTATTTTGGCAATATCCAAAGAGCTGATTCCTGAGTAG	17220
QY	17221	CACCTAATAATAGTTTAAACTGAGCATTTTCCGTTGAAACATACATTCATATTAGA	17280
Db	17221	CACCTAATAATAGTTTAAACTGAGCATTTTCCGTTGAAACATACATTCATATTAGA	17280
QY	17281	AAATAAAAGATCTTTGACAAATTTATTTTGTATCTTTTGTGCTGCTGCTGCTGCTGCTG	17340
Db	17281	AAATAAAAGATCTTTGACAAATTTATTTTGTATCTTTTGTGCTGCTGCTGCTGCTGCTG	17340
QY	17341	TGATAAATTAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAG	17400
Db	17341	TGATAAATTAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAG	17400
QY	17401	AACATCATATTTCTG	17460
Db	17401	AACATCATATTTCTG	17460
QY	17461	TATCACAATTTGATTTATATATCTTAAACATGTTGATTTGATTTGATTTGATTTGATTTG	17520
Db	17461	TATCACAATTTGATTTATATATCTTAAACATGTTGATTTGATTTGATTTGATTTGATTTG	17520
QY	17521	CAAAATAGAAAAACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	17580
Db	17521	CAAAATAGAAAAACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	17580
QY	17581	CTTGGCAAAACCTAGTGTGGGTAGAAATTTCTGCTTAAACAAACCTGCGTGGGTGGCT	17640
Db	17581	CTTGGCAAAACCTAGTGTGGGTAGAAATTTCTGCTTAAACAAACCTGCGTGGGTGGCT	17640
QY	17641	TGTGAGTGAACAACTGACAACTGTATGCAATGCGCTGCTTCTGATCTATAGATA	17700
Db	17641	TGTGAGTGAACAACTGACAACTGTATGCAATGCGCTGCTTCTGATCTATAGATA	17700
QY	17701	TTAAGCATTTGCAACAAAGAAATCTAAGAATGACATCTCTGATCTCTCTCTCTCTCTCT	17760
Db	17701	TTAAGCATTTGCAACAAAGAAATCTAAGAATGACATCTCTGATCTCTCTCTCTCTCTCT	17760

QY	17761	CCCTGAATTGCATGTCAGGACCTCCAGTTGACAGTTCACAGCCACAAATTTCCCTCCACA	17820		18841		18900
Db	17761	CCCTGAATTGCATGTCAGGACCTCCAGTTGACAGTTCACAGCCACAAATTTCCCTCCACA	17820		18901	TTATGTTTCTCTTTGGACATATATAAATGATTATCAAGGGATATGTCAGTGGGACT	18900
QY	17821	GGCTGTCAGGAGGACGTCGAAAGAACACACATTTGGCCAACTTCAGCTCTCTCT	17880		18901	TCTATGAATCAAAACACCAATATTTTCAAGCTAAGTCTAATAATTTTACTTTGAATTT	18960
Db	17821	GGCTGTCAGGAGGACGTCGAAAGAACACACATTTGGCCAACTTCAGCTCTCTCT	17880		18901	TCTATGAATCAAAACACCAATATTTTCAAGCTAAGTCTAATAATTTTACTTTGAATTT	18960
QY	17881	TATATTGACCGAGTAATTCCTGGGAGTCAACTGTAAAGCTTTGGCATCATCATTCAGGCT	17940		18961	CAATTCGCATTTATTTGTGTACATAAATTAGATTTTGTTCGTTGTTCTTCAAGTCCATCCA	19020
Db	17881	TATATTGACCGAGTAATTCCTGGGAGTCAACTGTAAAGCTTTGGCATCATCATTCAGGCT	17940		18961	CAATTCGCATTTATTTGTGTACATAAATTAGATTTTGTTCGTTGTTCTTCAAGTCCATCCA	19020
QY	17941	ATCCAGGTCAACTGTAAGCAATACATGCATCTGTGTAAGCAACACACAGTAAAGCAAA	18000		19021	ATTATCCATCATTTGGCAGGCAAAATCCTCTTATTGTTGGTCATACATAGTATCTTC	19080
Db	17941	ATCCAGGTCAACTGTAAGCAATACATGCATCTGTGTAAGCAACACACAGTAAAGCAAA	18000		19021	ATTATCCATCATTTGGCAGGCAAAATCCTCTTATTGTTGGTCATACATAGTATCTTC	19080
QY	18001	TTGCTCAGCATGTGTTTGGGGAATAGAGTGGGAAGATTTCTGTGAGGACAACTTTAATCC	18060		19081	TCACAAGAACACAGTTAGAAGCAAGTCTTTTGTCTGCACAGAACCCACCCCTTTCCC	19140
Db	18001	TTGCTCAGCATGTGTTTGGGGAATAGAGTGGGAAGATTTCTGTGAGGACAACTTTAATCC	18060		19081	TCACAAGAACACAGTTAGAAGCAAGTCTTTTGTCTGCACAGAACCCACCCCTTTCCC	19140
QY	18061	TGGGATTAATCCATCCTCAGGCTCTCAATTACTGGGAACCTTAAAGTAAAGACCTAATTT	18120		19141	AATGCACGCCCTTGTGTGCACAGCCACACAGAGGAATCCCATGAATGTTAGGCAGT	19200
Db	18061	TGGGATTAATCCATCCTCAGGCTCTCAATTACTGGGAACCTTAAAGTAAAGACCTAATTT	18120		19141	AATGCACGCCCTTGTGTGCACAGCCACACAGAGGAATCCCATGAATGTTAGGCAGT	19200
QY	18121	TCTCTCTTGATCCCATCTACCCCTTTGAAATAACACAAACAAACAAACAAACAAAC	18180		19201	TATCACCATGTTCTAATCTTAAACTCTAGCCCTGGTAAATGTTTAGGCTTAAACTGAACT	19260
Db	18121	TCTCTCTTGATCCCATCTACCCCTTTGAAATAACACAAACAAACAAACAAACAAAC	18180		19201	TATCACCATGTTCTAATCTTAAACTCTAGCCCTGGTAAATGTTTAGGCTTAAACTGAACT	19260
QY	18181	TTGGCTAAATTCATGTTCTGGTCAAAATTTCCCTTGCATCTTTTATGCAAAAAGTT	18240		19261	GCTTAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	19320
Db	18181	TTGGCTAAATTCATGTTCTGGTCAAAATTTCCCTTGCATCTTTTATGCAAAAAGTT	18240		19261	GCTTAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	19320
QY	18241	CAGAGGAAAGAAATGAAACATTTGGCAAAATTAATAATTAATGTCCTTTATCTCAAAAAG	18300		19321	TCAGTAGAATGCATCTAAGGAAATTTGCAGGAACAAAGTGTGACCATGAGTCCACTAAC	19380
Db	18241	CAGAGGAAAGAAATGAAACATTTGGCAAAATTAATAATTAATGTCCTTTATCTCAAAAAG	18300		19321	TCAGTAGAATGCATCTAAGGAAATTTGCAGGAACAAAGTGTGACCATGAGTCCACTAAC	19380
QY	18301	CAAAATAAAGTCTCTTCAATCTAAATTAATTAATTAATTAATTAATTAATTAATTAAT	18360		19381	GCATCCCTGTTGCTTTTATATCTACAACCTGCTTTGATCTCAAGGGCAGGAGTAT	19440
Db	18301	CAAAATAAAGTCTCTTCAATCTAAATTAATTAATTAATTAATTAATTAATTAATTAAT	18360		19381	GCATCCCTGTTGCTTTTATATCTACAACCTGCTTTGATCTCAAGGGCAGGAGTAT	19440
QY	18361	ATTTAAATATATCTAGACACATTTAGAGAACACCTGATATATATTTTACCTGCGACGT	18420		19441	ATCCCAATTTGTCATACCTGAGCCAGGATCTGTGGAACTAAATTAATGTCGCAAAATA	19500
Db	18361	ATTTAAATATATCTAGACACATTTAGAGAACACCTGATATATATTTTACCTGCGACGT	18420		19441	ATCCCAATTTGTCATACCTGAGCCAGGATCTGTGGAACTAAATTAATGTCGCAAAATA	19500
QY	18421	AAATTTCAACATAAATGTAATAAGAAAGGTTTATTTTAACTTCAAAAGT	18480		19501	TCAGTGTGCAATAATTTATTTGCTGTTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTT	19560
Db	18421	AAATTTCAACATAAATGTAATAAGAAAGGTTTATTTTAACTTCAAAAGT	18480		19501	TCAGTGTGCAATAATTTATTTGCTGTTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTT	19560
QY	18481	TAATCAACATGTTAGAGAAATGATTTTGTGTGATGATGATGATGATGATGATGATGATG	18540		19561	GCTATAATCAATCCAGATTTTAAATTTGAATGAACCTGCTTGGGAAAGGAACTTTTAT	19620
Db	18481	TAATCAACATGTTAGAGAAATGATTTTGTGTGATGATGATGATGATGATGATGATGATG	18540		19561	GCTATAATCAATCCAGATTTTAAATTTGAATGAACCTGCTTGGGAAAGGAACTTTTAT	19620
QY	18541	TGGGTCTAGATGGGAGTATAGCATAGTGTGATGATGATGATGATGATGATGATGATGATG	18600		19621	TGCTGTCAAAAGCCTGAAATAAATCTGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG	19680
Db	18541	TGGGTCTAGATGGGAGTATAGCATAGTGTGATGATGATGATGATGATGATGATGATGATG	18600		19621	TGCTGTCAAAAGCCTGAAATAAATCTGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG	19680
QY	18601	AATGCTCTCAATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	18660		19681	AGAAAGTGAGCAATCATCCATTACAAGTGTCAACCTTGAAGTAAATTAATTAATTAATTA	19740
Db	18601	AATGCTCTCAATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	18660		19681	AGAAAGTGAGCAATCATCCATTACAAGTGTCAACCTTGAAGTAAATTAATTAATTAATTA	19740
QY	18661	CTGAATCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT	18720		19741	TGCATTTCTGGGCTTGTGAACAGGCTGATCAGAGGCGCAAAATCTGCTGCTGCTGCTGCT	19800
Db	18661	CTGAATCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT	18720		19741	TGCATTTCTGGGCTTGTGAACAGGCTGATCAGAGGCGCAAAATCTGCTGCTGCTGCTGCT	19800
QY	18721	CTGACTCAATGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	18780		19801	TGGGAAGATATTTGCTTAACACGAGGAGTAAAGAGGTACAAATTAGCAGGAGGAGTCT	19860
Db	18721	CTGACTCAATGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	18780		19801	TGGGAAGATATTTGCTTAACACGAGGAGTAAAGAGGTACAAATTAGCAGGAGGAGTCT	19860
QY	18781	TTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	18840		19861	GATGTGTGAGAGGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	19920
Db	18781	TTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	18840		19861	GATGTGTGAGAGGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	19920
QY	18841	TTATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	18900		19921	TTGAGGCTCTGCTGAACTATGTCATACCTTACAGATATGACTACATTTAGTTGTTCTCC	19980
Db	18841	TTATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	18900		19921	TTGAGGCTCTGCTGAACTATGTCATACCTTACAGATATGACTACATTTAGTTGTTCTCC	19980

Db	19921	TTCAGCCCTCTGCTGAACATATGTCATAAACCTTACAGATATAGCTACATTTAGTTGTTCC	19981
Qy	19981	CACCCATTTCAAGTGAGTATTTATTTGCTTAAGAGTTTAAACAGTAAATGGTAAACACTGGAATT	20040
Db	19981	CACCCATTTCAAGTGAGTATTTATTTGCTTAAGAGTTTAAACAGTAAATGGTAAACACTGGAATT	20040
Qy	20041	GAAGCCTTTCGCCCTTTTTCCTCCATAGTCTCTGTCCACTTAAAGCAGAAATAGAGGGATGGT	20100
Db	20041	GAAGCCTTTCGCCCTTTTTCCTCCATAGTCTCTGTCCACTTAAAGCAGAAATAGAGGGATGGT	20100
Qy	20101	CAGTAAGCCATTAAGTTGAAGGAGAGACACAGTGTTATGAGGGCTGTACTGGACTTTCT	20160
Db	20101	CAGTAAGCCATTAAGTTGAAGGAGAGACACAGTGTTATGAGGGCTGTACTGGACTTTCT	20160
Qy	20161	GTCTGATGTTGAACACAGGGTGGGTGCTCAATGGCCACATCCTTATCTTCAGAAGACACC	20220
Db	20161	GTCTGATGTTGAACACAGGGTGGGTGCTCAATGGCCACATCCTTATCTTCAGAAGACACC	20220
Qy	20221	CAAGCCAAAGTACAGCATGCCCTTCCCTATAGGAAATCCCAATAAACTCCAAAGTGCCCTCC	20280
Db	20221	CAAGCCAAAGTACAGCATGCCCTTCCCTATAGGAAATCCCAATAAACTCCAAAGTGCCCTCC	20280
Qy	20281	ACAAACACGAGAGAGCATGTAGCCCTCATTTCTTAAACCAACCTCCACATTTGTA	20340
Db	20281	ACAAACACGAGAGAGCATGTAGCCCTCATTTCTTAAACCAACCTCCACATTTGTA	20340
Qy	20341	TAACTCTTTGACTAGCATTTGGTTACTTTTCAATTTCTTACTCACCATGAGGAGATTCACAAT	20400
Db	20341	TAACTCTTTGACTAGCATTTGGTTACTTTTCAATTTCTTACTCACCATGAGGAGATTCACAAT	20400
Qy	20401	TCGTGCAGTTTATGCATCAATTCACATAATGTCTACTAAGAACTGTGACCCAGTGTGACTG	20460
Db	20401	TCGTGCAGTTTATGCATCAATTCACATAATGTCTACTAAGAACTGTGACCCAGTGTGACTG	20460
Qy	20461	CTGTAGAATCCACCTGCCCTACATATACGCGCATTGAATACCCGAGCAGCTCAATTTAG	20520
Db	20461	CTGTAGAATCCACCTGCCCTACATATACGCGCATTGAATACCCGAGCAGCTCAATTTAG	20520
Qy	20521	AATTAGAACCTGAAAGGTTGTTCTGACTGGATGCAAAATTAACTTCAAAGCGTGATTCGACAG	20580
Db	20521	AATTAGAACCTGAAAGGTTGTTCTGACTGGATGCAAAATTAACTTCAAAGCGTGATTCGACAG	20580
Qy	20581	TTTTCTGAGGGGATATTGAGTTTCCAGTCAAAAGACATGATAAGCCAGTGCAGCAGAGC	20640
Db	20581	TTTTCTGAGGGGATATTGAGTTTCCAGTCAAAAGACATGATAAGCCAGTGCAGCAGAGC	20640
Qy	20641	AGGAGCCAGACAGAGGCTGAGCAGCAATTAAGGTTTCTGGTGCTTGGGTAGAGGAGA	20700
Db	20641	AGGAGCCAGACAGAGGCTGAGCAGCAATTAAGGTTTCTGGTGCTTGGGTAGAGGAGA	20700
Qy	20701	ATTCTAGAGTGAGACTTCTGGAGGGAGACAGCCAAAGTGTGTCAACCCGAGAGAGAGGG	20760
Db	20701	ATTCTAGAGTGAGACTTCTGGAGGGAGACAGCCAAAGTGTGTCAACCCGAGAGAGAGGG	20760
Qy	20761	GTGCGCCTTTCCTGCTGCATCAGTCTCCATAGCTGAACATTCAGAGCATCAAGGGTGT	20820
Db	20761	GTGCGCCTTTCCTGCTGCATCAGTCTCCATAGCTGAACATTCAGAGCATCAAGGGTGT	20820
Qy	20821	TCCAAATTTAATTCAGGGCCCGCTAATTTTCAACTTAACGTCCCTTATTTTCATCCAGTCT	20880
Db	20821	TCCAAATTTAATTCAGGGCCCGCTAATTTTCAACTTAACGTCCCTTATTTTCATCCAGTCT	20880
Qy	20881	ACATCATGGAATAATCCCTCTTTTCTGTGTCATTCGAAATTTAGTTTTGCTTTATCAAG	20940
Db	20881	ACATCATGGAATAATCCCTCTTTTCTGTGTCATTCGAAATTTAGTTTTGCTTTATCAAG	20940
Qy	20941	CTCTTTTGACATCAATTAAGTTTTTTTGGGCCCTCATACAGCGAGTTTCTTGGAAAGGCTGGG	21000
Db	20941	CTCTTTTGACATCAATTAAGTTTTTTTGGGCCCTCATACAGCGAGTTTCTTGGAAAGGCTGGG	21000
Qy	21001	AAGGCTCCCTGTCTCTCAAAAACCTCTCTTTGGACATACATGCTGTAAGTGTGGGGTGTGCA	21060
Db	21001	AAGGCTCCCTGTCTCTCAAAAACCTCTCTTTGGACATACATGCTGTAAGTGTGGGGTGTGCA	21060

QY	21061	CAGTGCACAGGGCGCACCCTTTTCCTTGCTGACGCCCTGCCTCTAGGTGCGCACGCTAAATCACAC	21120
DB	21061	CAGTGCACAGGGCGCACCCTTTTCCTTGCTGACGCCCTGCCTCTAGGTGCGCACGCTAAATCACAC	21120
QY	21121	GAGGTGCTTTTGAGATGTATAAAGAATGCTTGGGATCTGAGCTTAGAANTGGGATGTGAAT	21180
DB	21121	GAGGTGCTTTTGAGATGTATAAAGAATGCTTGGGATCTGAGCTTAGAANTGGGATGTGAAT	21180
QY	21181	GCACACCCCTTTTATAGTTTCTTAATATTAGTGTGGGAGGAAGGAGAGTCAACCTGTGTCCT	21240
DB	21181	GCACACCCCTTTTATAGTTTCTTAATATTAGTGTGGGAGGAAGGAGAGTCAACCTGTGTCCT	21240
QY	21241	TTTGATCCTGGCCACTTAGACTACTAAGTGCTGTGTTTCATCATGATGAGTGCATGAAATPACTC	21300
DB	21241	TTTGATCCTGGCCACTTAGACTACTAAGTGCTGTGTTTCATCATGATGAGTGCATGAAATPACTC	21300
QY	21301	ATAAATGCTATGAATTACATACAATCATTTACTCTTACTTTTGCAGTTGAGGAACACTGACC	21360
DB	21301	ATAAATGCTATGAATTACATACAATCATTTACTCTTACTTTTGCAGTTGAGGAACACTGACC	21360
QY	21361	CTTTTCAAAGCTTAAGAAAAAATAAAAAAAAAAAGCTTGCCACAGCCATACACCAAGTCAGTG	21420
DB	21361	CTTTTCAAAGCTTAAGAAAAAATAAAAAAAAAAAGCTTGCCACAGCCATACACCAAGTCAGTG	21420
QY	21421	GTAGAGCCAGAGTTTGAATCCAGGCCTCTTCATFGCCTTTTGTACATTTATGAGCCGAGTGT	21480
DB	21421	GTAGAGCCAGAGTTTGAATCCAGGCCTCTTCATFGCCTTTTGTACATTTATGAGCCGAGTGT	21480
QY	21481	AAGATTTGAAGAGGGTTCCAGAGACAGCTTCCACAAGCGATGCTGAAGTCTTCCCACC	21540
DB	21481	AAGATTTGAAGAGGGTTCCAGAGACAGCTTCCACAAGCGATGCTGAAGTCTTCCCACC	21540
QY	21541	AGAGGACCACTTGTCTGTGCAAAATGAGCTTGCTTCCTAGGTGACCCCATAGGCACCTAACCT	21600
DB	21541	AGAGGACCACTTGTCTGTGCAAAATGAGCTTGCTTCCTAGGTGACCCCATAGGCACCTAACCT	21600
QY	21601	GTCATTTTCAAAATGTCATTAATPACACATACCCAAGCAGCAGCAGTGTGTATCCTCATFC	21660
DB	21601	GTCATTTTCAAAATGTCATTAATPACACATACCCAAGCAGCAGCAGTGTGTATCCTCATFC	21660
QY	21661	CACCTATTTCAGTCTGACTAATAAAGCAGGCAGCTATTTCAGAGTCTACTTTTTGCTCTTGG	21720
DB	21661	CACCTATTTCAGTCTGACTAATAAAGCAGGCAGCTATTTCAGAGTCTACTTTTTGCTCTTGG	21720
QY	21721	TATTGTCATAAAAACATTTTCGTCTCTTTTATCTGAACCGAGTGGACTTTGGCCAAATGCACAC	21780
DB	21721	TATTGTCATAAAAACATTTTCGTCTCTTTTATCTGAACCGAGTGGACTTTGGCCAAATGCACAC	21780
QY	21781	TCITTCTTTTGTCTCAFTTCTCCTTTGAAACCCCTTTCTTGCCCTCATCTAGGAGCTGAATGG	21840
DB	21781	TCITTCTTTTGTCTCAFTTCTCCTTTGAAACCCCTTTCTTGCCCTCATCTAGGAGCTGAATGG	21840
QY	21841	ATTGATAGCAATGATTTGTCTCAGTGGGAACAAATGCCAGGATTCCTAAGATTTCTAGTTF	21900
DB	21841	ATTGATAGCAATGATTTGTCTCAGTGGGAACAAATGCCAGGATTCCTAAGATTTCTAGTTF	21900
QY	21901	TCGTAGGACAGATAAAACCAATATAATTTTCACATCTTGGCAGACACACATGGGTG	21960
DB	21901	TCGTAGGACAGATAAAACCAATATAATTTTCACATCTTGGCAGACACACATGGGTG	21960
QY	21961	GTGATCAGCTTAAGATAAAAAATTTAAAAATCTATTCTTTATTAAGTGAACATATTTAT	22020
DB	21961	GTGATCAGCTTAAGATAAAAAATTTAAAAATCTATTCTTTATTAAGTGAACATATTTAT	22020
QY	22021	TATTTTATACAAGTTACTTGTTCTGCTGGACAGAGTCAAAATGTGCCCTTACTTGGGTCAA	22080
DB	22021	TATTTTATACAAGTTACTTGTTCTGCTGGACAGAGTCAAAATGTGCCCTTACTTGGGTCAA	22080
QY	22081	AATCAAGGTATGTAAGGTAAAGTCTCTTTTGTGAATACAAAAATTCATTTATGAAACAAA	22140
DB	22081	AATCAAGGTATGTAAGGTAAAGTCTCTTTTGTGAATACAAAAATTCATTTATGAAACAAA	22140

Qy	22141	ATAATCTCCACCTTTGGAACATGGGAAGACACCTTTGGTTCTCCACATGCACAATTAATTTA	22200
Db	22141	ATAATCTCCACCTTTGAACATGGGAAGACACCTTTGGTTCTCCACATGCACAATTAATTTA	22200
Qy	22201	CTGCTGTTTGTGTCAACAGAGAGATGGTTTCTCTGAGTCAGTCTCTAAACATAAAGTTA	22260
Db	22201	CTGCTGTTTGTGTCAACAGAGAGATGGTTTCTCTGAGTCAGTCTCTAAACATAAAGTTA	22260
Qy	22261	TCAGTTGGCTTTTCACTGTGCTGGCCATTCAATCAATCTTTATTTCTGATAGTAACATACAT	22320
Db	22261	TCAGTTGGCTTTTCACTGTGCTGGCCATTCAATCAATCTTTATTTCTGATAGTAACATACAT	22320
Qy	22321	GCATTTTCTCTGTGATCATCCACAGACTCTCAGAGAAATCCAAATTAACCTGCTGCATGTCC	22380
Db	22321	GCATTTTCTCTGTGATCATCCACAGACTCTCAGAGAAATCCAAATTAACCTGCTGCATGTCC	22380
Qy	22381	TTGAAGACAGCTAGTAATCTTTTCTTTCTTTCTTTCTTTCTTTTGTGAGACAGAGTCTT	22440
Db	22381	TTGAAGACAGCTAGTAATCTTTTCTTTCTTTCTTTCTTTCTTTTGTGAGACAGAGTCTT	22440
Qy	22441	GCCTGCTGCCAGGCTGGAGTGCAGTGGCATGATTTCAGCTCACCATAACTTTCGGCTC	22500
Db	22441	GCCTGCTGCCAGGCTGGAGTGCAGTGGCATGATTTCAGCTCACCATAACTTTCGGCTC	22500
Qy	22501	CCAGGTTTAAGCAATTTCTCCCGCCTCAGCGCTTCTGAGTAGCTGGACACAGGTGTGTGC	22560
Db	22501	CCAGGTTTAAGCAATTTCTCCCGCCTCAGCGCTTCTGAGTAGCTGGACACAGGTGTGTGC	22560
Qy	22561	CACATGCCAGCTAAATTTTGTATTTTCAATTAGAGATAGAGTTTCAACATGTTGGCACCA	22620
Db	22561	CACATGCCAGCTAAATTTTGTATTTTCAATTAGAGATAGAGTTTCAACATGTTGGCACCA	22620
Qy	22621	GTAATCATTTTATGTGTTTCAAGGCTCAGGCTTTATAAGTCTAAAGTCTTTTATTAAC	22680
Db	22621	GTAATCATTTTATGTGTTTCAAGGCTCAGGCTTTATAAGTCTAAAGTCTTTTATTAAC	22680
Qy	22681	TCTTAGCAGCATGCAGCAGCGCTACACTAGTGCATATTTACCACATGGTGATGGC	22740
Db	22681	TCTTAGCAGCATGCAGCAGCGCTACACTAGTGCATATTTACCACATGGTGATGGC	22740
Qy	22741	ATGTGGAGATGAGCACTCAAGTAGGCGCATGATGTTTGAACACCATGCTCTGTTC	22800
Db	22741	ATGTGGAGATGAGCACTCAAGTAGGCGCATGATGTTTGAACACCATGCTCTGTTC	22800
Qy	22801	TTCTGTTTTGCTTTCTCTGGCATCTCAGCTTGCTATATATTTTAACTTCTAGAGCTCA	22860
Db	22801	TTCTGTTTTGCTTTCTCTGGCATCTCAGCTTGCTATATATTTTAACTTCTAGAGCTCA	22860
Qy	22861	AGTCAAAAGGCATATTCACCTCTACATCTCCTATGACTCGTCTCTATGTACTCACACAC	22920
Db	22861	AGTCAAAAGGCATATTCACCTCTACATCTCCTATGACTCGTCTCTATGTACTCACACAC	22920
Qy	22921	TTTTCTCGCCTCTATATAGCATTTTACTTTCATAGACCTTGTTTGTGTTTTCTTTCAGAT	22980
Db	22921	TTTTCTCGCCTCTATATAGCATTTTACTTTCATAGACCTTGTTTGTGTTTTCTTTCAGAT	22980
Qy	22981	AGTCCAACTTACAATGGTTTCAACATGAGTTTTTTTTTTTACTTTTTTGATGGTGTTC	23040
Db	22981	AGTCCAACTTACAATGGTTTCAACATGAGTTTTTTTTTTTACTTTTTTGATGGTGTTC	23040
Qy	23041	AGCTGTGATGTTTAAATGGTGAGCACCCATTAACCATTCGTGTTTTCTACTTTTCAGTAAG	23100
Db	23041	AGCTGTGATGTTTAAATGGTGAGCACCCATTAACCATTCGTGTTTTCTACTTTTCAGTAAG	23100
Qy	23101	TATTCAAATAATATATGAGCTATTAAACCTCTATTATAAAATAGGCTTTTGGTAGATA	23160
Db	23101	TATTCAAATAATATATGAGCTATTAAACCTCTATTATAAAATAGGCTTTTGGTAGATA	23160
Qy	23161	ATACTGACCACTATAGGCTGATATATGGTTCTCAACATGTTTAAAGTAGGCTAGGCTT	23220
Db	23161	ATACTGACCACTATAGGCTGATATATGGTTCTCAACATGTTTAAAGTAGGCTAGGCTT	23220
Qy	23221	AGCTAGCAAGTTTCAGTAGGCTATGTATTAAGTGGTTTGTGACTTAACTATATTTTCCA	23280

Db	23221		AGCTACGAAGTTCAGTAGGCTATGCTGATTTGAATGTGGTTTGACCTAACTATATTTTCCA	23280
Qy	23281	ATTACAATGTGTTTATTGGGATCTAAACCCATCAAAAGTTAAGAAGCATCCATATTCAGG	23340	
Db	23281	ATTACAATGTGTTTATTGGGATCTAAACCCATCAAAAGTTAAGAAGCATCCATATTCAGG	23340	
Qy	23341	TGCTTCCTCTCTATTTGAACCTAAAAAAGTTGTTGGAGGTAGAGAGCTAATCATCTTTTAT	23400	
Db	23401	CCCTTCCTCTCTAGTACTTTGTCCTTAATGTAAGGACCAAAATGCAGCTCATTTCAAGCTCA	23460	
Qy	23461	CTTCTAAACCATTTGACTTTCACGATTAGGACGAAGTGTCTGCTGAAGGACGACAACA	23520	
Db	23461	CTTCTAAACCATTTGACTTTCACGATTAGGACGAAGTGTCTGCTGAAGGACGACAACA	23520	
Qy	23521	TCGTCCTTTGGCCAGATTCCTTTGCAAGNAATAGACACTCAATTAATTACTACCTGAATG	23580	
Db	23521	TCGTCCTTTGGCCAGATTCCTTTGCAAGNAATAGACACTCAATTAATTACTACCTGAATG	23580	
Qy	23581	AATCAGATAAACCATGGATTTTTTCAGTTTAAATTTTTATCACAAGGTGAAACAATTCC	23640	
Db	23581	AATCAGATAAACCATGGATTTTTTCAGTTTAAATTTTTATCACAAGGTGAAACAATTCC	23640	
Qy	23641	AACATCTTTCAGGAATGCATAGAGTATTTAAATACCTTTATATCTTGAATGTTTGGATC	23700	
Db	23641	AACATCTTTCAGGAATGCATAGAGTATTTAAATACCTTTATATCTTGAATGTTTGGATC	23700	
Qy	23701	TTATCTCAAGACTAGTCTAGGATGTGCTAGTGGCGAAGCTTTAGGTTAGAATTAAGAA	23760	
Db	23701	TTATCTCAAGACTAGTCTAGGATGTGCTAGTGGCGAAGCTTTAGGTTAGAATTAAGAA	23760	
Qy	23761	ACTAGGATTTAGAACCATCTCTGCCAAGGATGAACCAAGATGCATGACTGGCACC	23820	
Db	23761	ACTAGGATTTAGAACCATCTCTGCCAAGGATGAACCAAGATGCATGACTGGCACC	23820	
Qy	23821	AAAGTCGTCAAAATATAGAGTGGCACACATGGTAGACATGGTCTCAGAAAGACTGGTT	23880	
Db	23821	AAAGTCGTCAAAATATAGAGTGGCACACATGGTAGACATGGTCTCAGAAAGACTGGTT	23880	
Qy	23881	CTCAGATGCAAAACATCAAGGTGCTAAGGAACATTCGCTTTGTCAAATGGGACAGTGCC	23940	
Db	23881	CTCAGATGCAAAACATCAAGGTGCTAAGGAACATTCGCTTTGTCAAATGGGACAGTGCC	23940	
Qy	23941	ATAATCTGTTATGAAAGTCTTAACATTTCCCTTTAATGTTGCAGACACAGGTTATGA	24000	
Db	23941	ATAATCTGTTATGAAAGTCTTAACATTTCCCTTTAATGTTGCAGACACAGGTTATGA	24000	
Qy	24001	TGCTTTGGGTGGGTGGAGGTGAGGGACTATAGGAATTAATGTAATTTTGTGTTAA	24060	
Db	24001	TGCTTTGGGTGGGTGGAGGTGAGGGACTATAGGAATTAATGTAATTTTGTGTTAA	24060	
Qy	24061	ACAACAGGGGCTCTCAGCCCTTCATAGGTTTCATAGTTCCACGAGGACTCTTCATCCTT	24120	
Db	24061	ACAACAGGGGCTCTCAGCCCTTCATAGGTTTCATAGTTCCACGAGGACTCTTCATCCTT	24120	
Qy	24121	ATGAATATTACAACCTCAGTGTGATTTTCAGAAATCCCTCTCTATAAATCAGCACATAAT	24180	
Db	24121	ATGAATATTACAACCTCAGTGTGATTTTCAGAAATCCCTCTCTATAAATCAGCACATAAT	24180	
Qy	24181	TATGAAACCTGTTTTTCCATTTCAATCCCAATGCAGAAAGTGCAGAAATAAATCTGGAAGGA	24240	
Db	24181	TATGAAACCTGTTTTTCCATTTCAATCCCAATGCAGAAAGTGCAGAAATAAATCTGGAAGGA	24240	
Qy	24241	CAATTATTTTAAAGTTTTTAATCAGGACTATCAGGATCTTTAACTTTAAATATATGAA	24300	
Db	24241	CAATTATTTTAAAGTTTTTAATCAGGACTATCAGGATCTTTAACTTTAAATATATGAA	24300	
Qy	24301	GACACTGAATTTTGTGACTCCACATGTGGGTTTAACTCTAAGGAATAAAAACATTTTACC	24360	



Db	24301	GACACTGAATTTTGTGACTCCACATGTGGTTTTAAACATCTAAAGAATAAAAAATTTACC	24360
QY	24361	ACTTGTGTTTACACAAATTAACCTAAATCACAGCAAAAGATCTTAATCAGACAATTCCT	24420
Db	24361	ACTTGTGTTTACACAAATTAACCTAAATCACAGCAAAAGATCTTAATCAGACAATTCCT	24420
QY	24421	GATTTTCAAGTTTGAAGCATTTGTGAAGCAAGGAGTGAATGAACTTTACTGAGCAACT	24480
Db	24421	GATTTTCAAGTTTGAAGCATTTGTGAAGCAAGGAGTGAATGAACTTTACTGAGCAACT	24480
QY	24481	ACTATCTATCCAGCACTTTGTGAGATGCTTTCACAAAAATCAAAATTTCAATTTCTCAC	24540
Db	24481	ACTATCTATCCAGCACTTTGTGAGATGCTTTCACAAAAATCAAAATTTCAATTTCTCAC	24540
QY	24541	AGCAAAACCTCATCTTTAGATATTACAAATTCCTGATGGATGATGAAGTGA	24600
Db	24541	AGCAAAACCTCATCTTTAGATATTACAAATTCCTGATGGATGATGAAGTGA	24600
QY	24601	GAGGACTTAAGTGACTTTGGCTTAAGCCACTGGACCTGAAGTGAATTCAGCACATATGA	24660
Db	24601	GAGGACTTAAGTGACTTTGGCTTAAGCCACTGGACCTGAAGTGAATTCAGCACATATGA	24660
QY	24661	CTGGAAAAATCAATGGATGACTGAATGAATATCTGGAAGGCACCTGAATTAGCCATGAAGC	24720
Db	24661	CTGGAAAAATCAATGGATGACTGAATGAATATCTGGAAGGCACCTGAATTAGCCATGAAGC	24720
QY	24721	AGTAACACCATCATAAAGCCATTTCTGAACCTGGGAATTCATGACCTGGGGTGATGA	24780
Db	24721	AGTAACACCATCATAAAGCCATTTCTGAACCTGGGAATTCATGACCTGGGGTGATGA	24780
QY	24781	TAAGCATATCTATGAATGAATAATTTTTTAAAAACAAGTTAGGAGATGAAGTCTTA	24840
Db	24781	TAAGCATATCTATGAATGAATAATTTTTTAAAAACAAGTTAGGAGATGAAGTCTTA	24840
QY	24841	AAATTTCTGTCTCTATTTACTAGACTATGAATCCCTGAGCTTTAAACACCATTTGAGTTG	24900
Db	24841	AAATTTCTGTCTCTATTTACTAGACTATGAATCCCTGAGCTTTAAACACCATTTGAGTTG	24900
QY	24901	CTCACAGCATGAGCTTTGCAGCCAAACAGGCCAAAGTTTCATGTCATGATTTCTTATTTTCT	24960
Db	24901	CTCACAGCATGAGCTTTGCAGCCAAACAGGCCAAAGTTTCATGTCATGATTTCTTATTTTCT	24960
QY	24961	AGCTCTCAGAAACTTCTGAAATTTTTTCTTTTACTATGCAAAAATGGGAATCACAGTA	25020
Db	24961	AGCTCTCAGAAACTTCTGAAATTTTTTCTTTTACTATGCAAAAATGGGAATCACAGTA	25020
QY	25021	GCCTCTGCCAAGGAACCTTGTAAAGATTAATGAGTTTTCAGTGTCTTGAAGCACAGTCTA	25080
Db	25021	GCCTCTGCCAAGGAACCTTGTAAAGATTAATGAGTTTTCAGTGTCTTGAAGCACAGTCTA	25080
QY	25081	AATCTCTACCTCTCAGTAGGTATGCCACATTTATTTACTGAAGTGAGTAAACACAGATCAAAG	25140
Db	25081	AATCTCTACCTCTCAGTAGGTATGCCACATTTATTTACTGAAGTGAGTAAACACAGATCAAAG	25140
QY	25141	AAGGAAGTTTAAATCAGAGCACCTAAAACCTAGAGGAGCTGAGATTCGTAAATGGTGA	25200
Db	25141	AAGGAAGTTTAAATCAGAGCACCTAAAACCTAGAGGAGCTGAGATTCGTAAATGGTGA	25200
QY	25201	TTACTAAGGAATAGAGGCCATGCCACCTTGAACCTAAATACAAAAAGCCAAATGATCAGG	25260
Db	25201	TTACTAAGGAATAGAGGCCATGCCACCTTGAACCTAAATACAAAAAGCCAAATGATCAGG	25260
QY	25261	TGTCCTTCAGTTTATACATCAGACGTAAACACTATCTTTTGAAGTGTATTTAGTCCATTC	25320
Db	25261	TGTCCTTCAGTTTATACATCAGACGTAAACACTATCTTTTGAAGTGTATTTAGTCCATTC	25320
QY	25321	TCATACGTAGATAAAGAACACCCAGAGCTGGTGGTATTTATAAGAAAAAGAGGTTTAAATG	25380
Db	25321	TCATACGTAGATAAAGAACACCCAGAGCTGGTGGTATTTATAAGAAAAAGAGGTTTAAATG	25380
QY	25381	GCCTCACACTTATGCAATTCCTGGGAGGCCCTAAGGAACTTACAATCATGGCAGAGGCG	25440
Db	25381	GCCTCACACTTATGCAATTCCTGGGAGGCCCTAAGGAACTTACAATCATGGCAGAGGCG	25440

QY	25441	AAAGGAAAGCAAGGACACGCTTTACATGCTGGCAGGAGGAGAGCATGTGTGCAAGTGTA	25500
Db	25441	AAAGGAAAGCAAGGACACGCTTTACATGCTGGCAGGAGGAGAGCATGTGTGCAAGTGTA	25500
QY	25501	GGGGAACCTGCCCTTTATAAATCATCAGATCTTGTGCCACTCCTCCTCATCATCACAAGAT	25560
Db	25501	GGGGAACCTGCCCTTTATAAATCATCAGATCTTGTGCCACTCCTCCTCATCATCACAAGAT	25560
QY	25561	AGCATGGGAAACCAATCCCATGATTCAAATATCTCCATCTTGTTCCTCCCTTGACATG	25620
Db	25561	AGCATGGGAAACCAATCCCATGATTCAAATATCTCCATCTTGTTCCTCCCTTGACATG	25620
QY	25621	TGGGATTTATGGGATTTATGGGATTTGCAATTTCAAGATGAGATTTGGGTGGGAGACAAAT	25680
Db	25621	TGGGATTTATGGGATTTATGGGATTTGCAATTTCAAGATGAGATTTGGGTGGGAGACAAAT	25680
QY	25681	GCATACTATATAGCAAGTAAAGACACCTCAGTGAGTTGGATCTCTCAGCACACAGCAGG	25740
Db	25681	GCATACTATATAGCAAGTAAAGACACCTCAGTGAGTTGGATCTCTCAGCACACAGCAGG	25740
QY	25741	CCTACAAGCATATATCTCTAGGAGCAGTGTAGTGTCTCCTTAAAGTCTAGTGGGCGATAA	25800
Db	25741	CCTACAAGCATATATCTCTAGGAGCAGTGTAGTGTCTCCTTAAAGTCTAGTGGGCGATAA	25800
QY	25801	AGSAAACCAATCCCATATTAATTTTCCAATGCTTCCAGAAAAAATTTAGCACAGCAAAAC	25860
Db	25801	AGSAAACCAATCCCATATTAATTTTCCAATGCTTCCAGAAAAAATTTAGCACAGCAAAAC	25860
QY	25861	ACAAGAACACACATTTCTCTTTAAACAAGTAATTTGCAGTGGAAAAATGCACATTTGTC	25920
Db	25861	ACAAGAACACACATTTCTCTTTAAACAAGTAATTTGCAGTGGAAAAATGCACATTTGTC	25920
QY	25921	ATCCGACGCTAAAAGTTTACCTATGGCTTCCACTGTCAACTGGATTTTCCCTATTGATTT	25980
Db	25921	ATCCGACGCTAAAAGTTTACCTATGGCTTCCACTGTCAACTGGATTTTCCCTATTGATTT	25980
QY	25981	GCATTTGAATGACATCCCTAGATGAGGGGAATAACTTTGATATAGGGTGGGGTTAGGA	26040
Db	25981	GCATTTGAATGACATCCCTAGATGAGGGGAATAACTTTGATATAGGGTGGGGTTAGGA	26040
QY	26041	TATCCAAAGACGCGCAACTGGCTAGGATGAAGAGAGAGGTGCGCAGGACAGGACAGGA	26100
Db	26041	TATCCAAAGACGCGCAACTGGCTAGGATGAAGAGAGAGGTGCGCAGGACAGGACAGGA	26100
QY	26101	GGAAAAACAACCTGAAAGTTGTCCACTGCTGAGATTTCTTAAATATTTTCATGTGTGTG	26160
Db	26101	GGAAAAACAACCTGAAAGTTGTCCACTGCTGAGATTTCTTAAATATTTTCATGTGTGTG	26160
QY	26161	CCCTCATAGACACACAAATATGATAAACAACAATATGTTTATGAATGCTTGTGTGC	26220
Db	26161	CCCTCATAGACACACAAATATGATAAACAACAATATGTTTATGAATGCTTGTGTGC	26220
QY	26221	AAACAGAGTAAGTGAGGAGCTAGATACCTACAAATCATATGAGTCAATAAACAGTGGCAA	26280
Db	26221	AAACAGAGTAAGTGAGGAGCTAGATACCTACAAATCATATGAGTCAATAAACAGTGGCAA	26280
QY	26281	AGTCTCTAAAAGAAAAGCTTAGCAGAAAAACATCCAATAAGCAAAATAGTGTGCAAAA	26340
Db	26281	AGTCTCTAAAAGAAAAGCTTAGCAGAAAAACATCCAATAAGCAAAATAGTGTGCAAAA	26340
QY	26341	ATTTCCTGGAATAATAGTATCAGAAAAAGTTTAGTACTTGGAGATAATTTTGAACCTTTTA	26400
Db	26341	ATTTCCTGGAATAATAGTATCAGAAAAAGTTTAGTACTTGGAGATAATTTTGAACCTTTTA	26400
QY	26401	ATGAGTACACTGATTTATACAGATAATTAATTAAGACAATATTTGCCAAATACTATCTGTG	26460
Db	26401	ATGAGTACACTGATTTATACAGATAATTAATTAAGACAATATTTGCCAAATACTATCTGTG	26460
QY	26461	AGGCTCTCCAGATTTACTGATGTTTCTTAGAGCCTTATAGGGAAGACAGACAGCAATTT	26520
Db	26461	AGGCTCTCCAGATTTACTGATGTTTCTTAGAGCCTTATAGGGAAGACAGACAGCAATTT	26520



QY	26521	AATAGAAATATCTTGGTCTGTGTCAGAGTTTTGCAAGCAATTCAAATAATAACAGTAGCT	26580		QY	27601	ATGTTTACTGCACCTCAATATTAAATACTGTTTTTCTGTTGTTGTTTTTGTGTTTTT	27660
Db	26521	AATAGAAATATCTTGGTCTGTGTCAGAGTTTTGCAAGCAATTCAAATAATAACAGTAGCT	26580		QY	27661	TTTTTAAAGCAGGGTCTTCACTCTGTTACACAGAGCTGGAGTGCAGTCAGTCACAGC	27720
QY	26581	ATCATTTATTGAGGGTGTAGATACCTTTTCATTTACCTTAATCCTAACACAAATTTGCCAA	26640		Db	27661	TTTTTAAAGCAGGGTCTTCACTCTGTTACACAGAGCTGGAGTGCAGTCAGTCACAGC	27720
Db	26581	ATCATTTATTGAGGGTGTAGATACCTTTTCATTTACCTTAATCCTAACACAAATTTGCCAA	26640		QY	27721	CCATGGTAGCCTTGAACCTACCGGGCTCAAGTGATCTCCACACCTCCAGCCTCCTCAGTAG	27780
QY	26641	GTGCTTATAATTTAGAGCCATTTTACAAAGAGAGAAATFAGAGAAATCAGGGGTCTGTAAG	26700		Db	27721	CCATGGTAGCCTTGAACCTACCGGGCTCAAGTGATCTCCACACCTCCAGCCTCCTCAGTAG	27780
Db	26641	GTGCTTATAATTTAGAGCCATTTTACAAAGAGAGAAATFAGAGAAATCAGGGGTCTGTAAG	26700		QY	27781	CTGGAACCTACAGGTATATGCTTTCACGGGTGCTAACTTTTGTATTTTGTAGACAGAG	27840
QY	26701	TGACTTCTCCAAGGCCACTGCTACTGATTTTAGGATTTGAGTTAGATTTTATTAACAAGT	26760		Db	27781	CTGGAACCTACAGGTATATGCTTTCACGGGTGCTAACTTTTGTATTTTGTAGACAGAG	27840
Db	26701	TGACTTCTCCAAGGCCACTGCTACTGATTTTAGGATTTGAGTTAGATTTTATTAACAAGT	26760		QY	27841	TTCCTCACCATGTTGCCAGGCTGGTCTCTCACTCTCGGCTCAAGCGATCTGCCCTACCTC	27900
QY	26761	TAGTTTGACTCTCAAGTCCATGCTCTTTCCATTGCAAGCTCCTCTTCTTTTGGTCTAT	26820		Db	27841	TTCCTCACCATGTTGCCAGGCTGGTCTCTCACTCTCGGCTCAAGCGATCTGCCCTACCTC	27900
Db	26761	TAGTTTGACTCTCAAGTCCATGCTCTTTCCATTGCAAGCTCCTCTTCTTTTGGTCTAT	26820		QY	27901	GGCCTCCCAAAAGTGTGGGATCAGACAGTGAAGCCACTGTGTGAGTCTTAAACACTTTT	27960
QY	26821	TTCTATTAAATTTATGCCAAACAATTTTAATATTGATAAATAAACTTTCACTTGGTAAA	26880		Db	27901	GGCCTCCCAAAAGTGTGGGATCAGACAGTGAAGCCACTGTGTGAGTCTTAAACACTTTT	27960
Db	26821	TTCTATTAAATTTATGCCAAACAATTTTAATATTGATAAATAAACTTTCACTTGGTAAA	26880		QY	27961	TAAAGAGAGGTGGATTTGAATTTTAGCATGTGTATCTTAAATAATGATTTACTTTTGGAGA	28020
QY	26881	GGTACCAATATATACCACATGGTTTCAGGAACTCAATGAAGCTAACCATCTTTCAATAATA	26940		Db	27961	TAAAGAGAGGTGGATTTGAATTTTAGCATGTGTATCTTAAATAATGATTTACTTTTGGAGA	28020
Db	26881	GGTACCAATATATACCACATGGTTTCAGGAACTCAATGAAGCTAACCATCTTTCAATAATA	26940		QY	28021	ACAATATATTTAATTTAATAATTTAAACTATTAATTTGGAAACACCCCAATAATTTGTT	28080
QY	26941	GAACCTATTATTAACAATAATGTAATATTAATGAACACACAGTAAGTTATTAATGCTTA	27000		Db	28021	ACAATATATTTAATTTAATAATTTAAACTATTAATTTGGAAACACCCCAATAATTTGTT	28080
Db	26941	GAACCTATTATTAACAATAATGTAATATTAATGAACACACAGTAAGTTATTAATGCTTA	27000		QY	28081	CATATTTTAAATCAAAACACAGCTTTGAAAACAGGTTTCCCTCTTGCATTTATGTCCTG	28140
QY	27001	TTATCTACTGATGTACCAGTACCCTTAATTTACAGAGATGTAGTTACAGATATCTGA	27060		Db	28081	CATATTTTAAATCAAAACACAGCTTTGAAAACAGGTTTCCCTCTTGCATTTATGTCCTG	28140
Db	27001	TTATCTACTGATGTACCAGTACCCTTAATTTACAGAGATGTAGTTACAGATATCTGA	27060		QY	28141	GATTTTCTTGGTGAACACACACTATCATTTCTAGAAAAGTCAAGTTCTCTCGGAATAAGAAA	28200
QY	27061	AGACTGACTGATCTGACTATCATCTGCTGTCGGCCAAACAGCTTTTGGCAAAATCTTAACC	27120		Db	28141	GATTTTCTTGGTGAACACACACTATCATTTCTAGAAAAGTCAAGTTCTCTCGGAATAAGAAA	28200
Db	27061	AGACTGACTGATCTGACTATCATCTGCTGTCGGCCAAACAGCTTTTGGCAAAATCTTAACC	27120		QY	28201	AAGAACAGATCTTACTTATATTGTTATCTCCATAAATCACTCTCCGTAAATGCCAGT	28260
QY	27121	CAAGTATCAATATAGCAGACAGAGAAATTCGAACCACTCAGTTTCTAAATATGTTTCAAT	27180		Db	28201	AAGAACAGATCTTACTTATATTGTTATCTCCATAAATCACTCTCCGTAAATGCCAGT	28260
Db	27121	CAAGTATCAATATAGCAGACAGAGAAATTCGAACCACTCAGTTTCTAAATATGTTTCAAT	27180		QY	28261	CAGGCTGATCATTTCTTAATTTAGAAATGTTGAATTTTATGCTATGAACCTTGAATAAT	28320
QY	27181	ATGTTAATGCTCTCTGTAATTTTCTACATTTGAAATCAATTTTGAATAATCAAACTT	27240		Db	28261	CAGGCTGATCATTTCTTAATTTAGAAATGTTGAATTTTATGCTATGAACCTTGAATAAT	28320
Db	27181	ATGTTAATGCTCTCTGTAATTTTCTACATTTGAAATCAATTTTGAATAATCAAACTT	27240		QY	28321	ATACATGCTCTTAAATTCATAGGTATATGTTTTTCTGTTTTGTTTTTGTGTTTTTAAT	28380
QY	27241	GTGTCCTCTGTTTAGCATGCGATGCGATGACAAAGAACAGCAATAATGATAAAATTT	27300		Db	28321	ATACATGCTCTTAAATTCATAGGTATATGTTTTTCTGTTTTGTTTTTGTGTTTTTAAT	28380
Db	27241	GTGTCCTCTGTTTAGCATGCGATGCGATGACAAAGAACAGCAATAATGATAAAATTT	27300		QY	28381	TTATGATTATTATATCTTTAAGTTTATAGATACATATGCACAATGTCGAGGTTTGTACAT	28440
QY	27301	TTTTAAAGAACCTATCTGACTTAAGAGAACTCAGAACGAATGAAGAACATCTGATATAA	27360		Db	28381	TTATGATTATTATATCTTTAAGTTTATAGATACATATGCACAATGTCGAGGTTTGTACAT	28440
Db	27301	TTTTAAAGAACCTATCTGACTTAAGAGAACTCAGAACGAATGAAGAACATCTGATATAA	27360		QY	28441	ATGATACATGTGCCATGTTGGTGTGTCGCCCATTAACCTGTCATTTAAACATTAGGTA	28500
QY	27361	AACATTATTTCATTTATTTCTCAGTTTCTTATGCTAGTTATTTACCTGTAATAATTTG	27420		Db	28441	ATGATACATGTGCCATGTTGGTGTGTCGCCCATTAACCTGTCATTTAAACATTAGGTA	28500
Db	27361	AACATTATTTCATTTATTTCTCAGTTTCTTATGCTAGTTATTTACCTGTAATAATTTG	27420		QY	28501	TATCTCTTAATGCTATCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT	28560
QY	27421	CAAAATAGAGTCAAAATGTTTAGATTTTAGAGGAAATGTCATGGAGAAATAATAGAAAT	27480		Db	28501	TATCTCTTAATGCTATCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT	28560
Db	27421	CAAAATAGAGTCAAAATGTTTAGATTTTAGAGGAAATGTCATGGAGAAATAATAGAAAT	27480		QY	28561	GTTCCCTCTCTGTGTCCTCATGTTCTCATTTGTTCAATTTCCACCTATGATGAGTGAACAAT	28620
QY	27481	TGGTATTAGATCCTTGGAAATGGTGGTGAAGTCTCCACAGTCTTAACATCTACCACTT	27540		Db	28561	GTTCCCTCTCTGTGTCCTCATGTTCTCATTTGTTCAATTTCCACCTATGATGAGTGAACAAT	28620
Db	27481	TGGTATTAGATCCTTGGAAATGGTGGTGAAGTCTCCACAGTCTTAACATCTACCACTT	27540		QY	28621	CGGTTGTTGTTTTTGTCTCTGTGATAGTTTGTCTGAGAAATGATGTTTCCAGCTTCAT	28680
QY	27541	TAGAGTCTGTAAAAATACATATTTCAACAGCTCATCTTTTGGAACTAATTTAGTATCAAG	27600		Db	28621	CGGTTGTTGTTTTTGTCTCTGTGATAGTTTGTCTGAGAAATGATGTTTCCAGCTTCAT	28680
Db	27541	TAGAGTCTGTAAAAATACATATTTCAACAGCTCATCTTTTGGAACTAATTTAGTATCAAG	27600		QY	28681	CCATGTCCTCAAAAGGACGAACTCATCATTTTATGCTGATGATATTCATTCATCGT	28740
QY	27601	ATGTTTACTGCACCTCAATATTAAATACTGTTTTTGTGTTGTTTTTGTGTTTTT	27660					



Db 1312 CAGGCTAGTAGTAAGTTGGTGGTAGGAAAAGGGTCTCTTATCTCACCCCTCCTTAA 1253  
QY 481 ACTAAAGGTCTCTTTCAGGCTTAATGTAAGGATGTGCACATCTCTTATCTCGAGGTGGTCTT 540  
Db 1252 ACTAAAGGTCTCTTTCAGGCTTAATGTAAGGATGTGCACATCTCTTATCTCGAGGTGGTCTT 1193  
QY 541 GAGCTGCAGATACAATACATCGTTTCATGGTGATCCAACTGGGATGTCAACTAGAGCCCATG 600  
Db 1192 GAGCTGCAGATACAATACATCGTTTCATGGTGATCCAACTGGGATGTCAACTAGAGCCCATG 1133  
QY 601 GTCTTAGCTCTACCCCTCTCTTGATGTGGCCAGGCTCAAACTGTAATACCT 652  
Db 1132 GTCTTAGCTCTACCCCTCTCTTGATGTGGCCAGGCTCAAACTGTAATACCT 1081

RESULT 3

US-10-258-557-1/c  
Sequence: 10258557  
Publication No. US20030300502A1  
GENERAL INFORMATION:  
APPLICANT: Beals, John  
APPLICANT: Gonzalez-DeWhitt, Patricia  
APPLICANT: Hammond, Lisa  
APPLICANT: Lu, Jirong  
APPLICANT: Na, Songqing  
APPLICANT: Su, Eric  
APPLICANT: Witcher, Derrick  
TITLE OF INVENTION: TREATING MUSCULOSKELETAL DISORDERS USING LP85 AND ANALOGS THEREOF  
FILE REFERENCE: X-14392M  
CURRENT APPLICATION NUMBER: US/10/258,557  
CURRENT FILING DATE: 2002-10-23  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 3736  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (114)..(1223)  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: (114)..(149)  
US-10-258-557-1

Query Match 2.2%; Score 652; DB 9; Length 3736;  
Best Local Similarity 100.0%; Pred. No. 1.3e-285;  
Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATATGTAAGAAAGCCCTCATCTTTTGATTTTAAATATACAGATGCTTCTTTAAAGAGA 60  
Db 1750 GTATATGTAAGAAAGCCCTCATCTTTTGATTTTAAATATACAGATGCTTCTTTAAAGAGA 1691  
QY 61 GCAAGATTCAAAATTTGTTGGTTTCAAAATTTTAAATATATCTCTCTAAATTTT 120  
Db 1690 GCAAGATTCAAAATTTGTTGGTTTCAAAATTTTAAATATATCTCTCTAAATTTT 1631  
QY 121 CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGCAGAGATTTTAAGAGTCT 180  
Db 1630 CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGCAGAGATTTTAAGAGTCT 1571  
QY 181 AACTCAAAACATATGTAAGCTCTGGTGTACCTGGTTATATATACCAAAAAACATTTGAT 240  
Db 1570 AACTCAAAACATATGTAAGCTCTGGTGTACCTGGTTATATATACCAAAAAACATTTGAT 1511  
QY 241 CTATATACATATGACATGAATATATTTCTGTGTGTTTGTGTCATATATACCTCAAC 300  
Db 1510 CTATATACATATGACATGAATATATTTCTGTGTGTTTGTGTCATATATACCTCAAC 1451  
QY 301 ACTATATTAATGCAATCCCTATTTCTTAGGTATAGAGTTGATGATATACCTTCTAC 360  
Db 1450 ACTATATTAATGCAATCCCTATTTCTTAGGTATAGAGTTGATGATATACCTTCTAC 1391

QY 361 TTGCCATGCGATTTACAAAGCAAGGCTGAGACTCAGCAACACCTTGTGTTCATTGCAATTG 420  
Db 1390 TTGCCATGCGATTTACAAAGCAAGGCTGAGACTCAGCAACACCTTGTGTTCATTGCAATTG 1331  
QY 421 CAGGCTAGTAGTAAGTTGGTGGTAGGAAAAGGCTCTCTTATCTCACCCCTCCTTAA 480  
Db 1330 CAGGCTAGTAGTAAGTTGGTGGTAGGAAAAGGCTCTCTTATCTCACCCCTCCTTAA 1271  
QY 481 ACTAAAGGTCTCTTTCAGGCTTAATGTAAGGATGTGCACATCTCTTATCTCGAGGTGGTCTT 540  
Db 1270 ACTAAAGGTCTCTTTCAGGCTTAATGTAAGGATGTGCACATCTCTTATCTCGAGGTGGTCTT 1211  
QY 541 GAGCTGCAGATACAATACATCGTTTCATGGTGATCCAACTGGGATGTCAACTAGAGCCCATG 600  
Db 1210 GAGCTGCAGATACAATACATCGTTTCATGGTGATCCAACTGGGATGTCAACTAGAGCCCATG 1151  
QY 601 GTCTTAGCTCTACCCCTCTCTTGATGTGGCCAGGCTCAAACTGTAATACCT 652  
Db 1150 GTCTTAGCTCTACCCCTCTCTTGATGTGGCCAGGCTCAAACTGTAATACCT 1099

RESULT 4

US-10-086-623-5/c  
Sequence: 10086623  
Publication No. US20020104740A1  
GENERAL INFORMATION:  
APPLICANT: ERIKSSON, Ulf  
APPLICANT: AASE, Karin  
APPLICANT: LI, Xuri  
APPLICANT: PONTE, Annica  
APPLICANT: UTELA, Marko  
APPLICANT: ALITALO, Kari  
APPLICANT: OESTMAN, Arne  
APPLICANT: HELDIN, Carl-Henrik  
TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES  
FILE REFERENCE: 1064/44833C2  
CURRENT APPLICATION NUMBER: US/10/086,623  
CURRENT FILING DATE: 2000-03-04  
PRIOR APPLICATION NUMBER: US 60/107,852  
PRIOR FILING DATE: 1998-11-10  
PRIOR APPLICATION NUMBER: US 60/113,997  
PRIOR FILING DATE: 1998-12-28  
PRIOR APPLICATION NUMBER: US 60/150,604  
PRIOR FILING DATE: 1999-08-26  
PRIOR APPLICATION NUMBER: US 60/157,108  
PRIOR FILING DATE: 1999-10-04  
PRIOR APPLICATION NUMBER: US 60/157,756  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 09/438,046  
PRIOR FILING DATE: 1999-11-10  
PRIOR APPLICATION NUMBER: US 09/691,200  
PRIOR FILING DATE: 2000-10-19  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 1934  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(966)  
OTHER INFORMATION:  
US-10-086-623-5

Query Match 2.0%; Score 601; DB 9; Length 1934;  
Best Local Similarity 99.8%; Pred. No. 2e-262;  
Matches 651; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTATATGTAAGAAAGCCCTCATCTTTTGATTTTAAATATACAGATGCTTCTTTAAAGAGA 60  
Db 1493 GTATATGTAAGAAAGCCCTCATCTTTTGATTTTAAATATACAGATGCTTCTTTAAAGAGA 1434

Qy	61	GCAAGATTCAAAATTTGTTTGTGTTTCAAAATTTAAATAAATTTATCTCCTAAATTTT	120
Db	1433	GCAAGATTCAAAATTTGTTTGTGTTTCAAAATTTAAATAAATTTATCTCCTAAATTTT	1374
Qy	121	CTAAAGACATGTTTCATATATTTGACCATCCCTTATTTTGCAGAAAGATTTTAAAGAGTCT	180
Db	1373	CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAGATTTTAAAGAGTCT	1314
Qy	181	AACTCAACATATGTAAGCTCTCGGTGTACCTGGTTATATATACCAAAAAAACAATTTGAT	240
Db	1313	AACTCAACATATGTAAGCTCTCGGTGTACCTGGTTATATATACCAAAAAAACAATTTGAT	1254
Qy	241	CTATATACACATAGACATGAATATATTTCTGTGTGTGTTTGTGCAATATAAACCCTCAAC	300
Db	1253	CTATATACACATAGACATGAATATATTTCTGTGTGTGTTTGTGCAATATAAACCCTCAAC	1194
Qy	301	ACTATTATTAATGCAATCCTATATCTTAGGTATAGAAGTTGATGATATACCTTCTCTAC	360
Db	1193	ACTATTATTAATGCAATCCTATATCTTAGGTATAGAAGTTGATGATATACCTTCTCTAC	1134
Qy	361	TTGCCATGGCATTAAACAAGCAAGGCTGAGACTCAGCAACCACTTGTGTTCATTGCATTG	420
Db	1133	TTGCCATGGCATTAAACAAGCAAGGCTGAGACTCAGCAACCACTTGTGTTCATTGCATTG	1074
Qy	421	CAGGCTAGTAGTAAGTTTGGTTGCTGTGTAGAAAAGGTCCTTATCTCACCTCCCTTAA	480
Db	1073	CAGGCTAGTAGTAAGTTTGGTTGCTGTGTAGAAAAGGTCCTTATCTCACCTCCCTTAA	1014
Qy	481	ACTAAAGGTTCTTTCAGGCTTAATGTAAGGATGTGCACATTCCTTATCAGGTGGTCTT	540
Db	1013	ACTAAAGGTTCTTTCAGGCTTAATGTAAGGATGTGCACATTCCTTATCAGGTGGTCTT	954
Qy	541	GAGCTGCAGATACAATGACATCTCATGTTGATCCAACTGGATGTCAACTAGAGCCATG	600
Db	953	GAGCTGCAGATACAATGACATCTCATGTTGATCCAACTGGATGTCAACTAGAGCCATG	894
Qy	601	GTCTTAGCTTACCCCTCTCTTGATGTGCCAGGCTCAAACTGTATACTT	652
Db	893	GTCTTAGCTTACCCCTCTCTTGATGTGCCAGGCTCAAACTGTATACTT	842

~~RESULT 5~~

RESULT 3  
US-10-260-539-5/c

03-10-200-333-3/C  
; Sequence 5, Application US/10260539; sequence 3, application 03/1020  
; Publication No. US20030073637A1

; FUDITION NO: 0320  
; GENERAL INFORMATION:

; APPLICANT: ERIKSSON, Ulf

; APPLICANT: AASE, Karin

APPLICANT: LI, XURI

APPLICANT: PONTEN, Annica

APPLICANT: UUTELA, Marko

APPLICANT: ALITALO, Kari

APPLICANT: OESTMAN, Arne

; APPLICANT: HELDIN, Carl-Henrik

PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES THEREOF

FILE REFERENCE: 1064/44833C2

; CURRENT APPLICATION NUMBER: US/10/260,539

2002-10-01

; PRIOR APPLICATION NUMBER: US/10/086,623

; PRIOR FILING DATE: 2000-03-04

; PRIOR APPLICATION NUMBER: US 60/107,852

; PRIOR FILING DATE: 1998-11-10

; PRIOR APPLICATION NUMBER: US 60/113,997

; PRIOR FILING DATE: 1998-12-28

; PRIOR APPLICATION NUMBER: US 60/150,604

; PRIOR FILING DATE: 1999-08-26

; PRIOR APPLICATION NUMBER: US 60/157,108

;; PRIOR FILING DATE: 1999-10-04

; PRIOR APPLICATION NUMBER: US 60/157,756

;  
; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: US 09/438,046

; PRIOR FILING DATE: 1999-11-10

; PRIOR APPLICATION NUMBER: US 09/691,200

## RESULT 6

~~US-10-086-623-7/c~~

03-10-080-023-77C  
: Sequence 7, Application US/10086623

; sequence /, Application of  
; Patent No. US20020164710A1

GENERAL INFORMATION:

; APPLICANT: ERIKSSON, Ulf

APPLICANT: AASE, Karin

APPLICANT: LI, Xuri

; APPLICANT: PONTEN, Annica

APPLICANT: UUTELA, Marko

; APPLICANT: ALITALO, Kari

APPLICANT: OESTMAN, Arne  
APPLICANT: HELDIN, Carl-Henrik  
TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES TH  
FILE REFERENCE: 1064/44833C2  
CURRENT APPLICATION NUMBER: US/10/086,623  
CURRENT FILING DATE: 2000-03-04  
PRIOR APPLICATION NUMBER: US 60/107,852  
PRIOR FILING DATE: 1998-11-10  
PRIOR APPLICATION NUMBER: US 60/113,997  
PRIOR FILING DATE: 1998-12-28  
PRIOR APPLICATION NUMBER: US 60/150,604  
PRIOR FILING DATE: 1999-08-26  
PRIOR APPLICATION NUMBER: US 60/157,108  
PRIOR FILING DATE: 1999-10-04  
PRIOR APPLICATION NUMBER: US 60/157,756  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 09/438,046  
PRIOR FILING DATE: 1999-11-10  
PRIOR APPLICATION NUMBER: US 09/691,200  
PRIOR FILING DATE: 2000-10-19  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7  
LENGTH: 2253  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (176)..(1288)  
OTHER INFORMATION:  
US-10-086-623-7

Query Match 2.0%; Score 601; DB 9; Length 2253;

Best Local Similarity 99.8%; Pred. No. 2e-262;

Matches 651; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTATATGTAAGAACGCTCATCTTTTGATTTTAAATACAAAGATGCTTTCTTAAGAGA 60  
DB 1812 GTATATGTAAGAACGCTCATCTTTTGATTTTAAATACAAAGATGCTTTCTTAAGAGA 1753  
QY 61 GCAAGATTCAAAATGTTTGTGTTTCAAAATTTTAAATTAATTTATCTCTAAATTTT 120  
DB 1752 GCAAGATTCAAAATGTTTGTGTTTCAAAATTTTAAATTAATTTATCTCTAAATTTT 1693  
QY 121 CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAGAGATTTTAAGAGTCT 180  
DB 1692 CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAGAGATTTTAAGAGTCT 1633  
QY 181 AACTCAACATATGTAAGCTCTGGTGACCTGGTTATATATACCAAAAAAACATTTGAT 240  
DB 1632 AACTCAACATATGTAAGCTCTGGTGACCTGGTTATATATACCAAAAAAACATTTGAT 1573  
QY 241 CTATATACATAGACATGAATATATTTCTGTGCTGTTTGGCATATATACCTCAAC 300  
DB 1572 CTATATACATAGACATGAATATATTTCTGTGCTGTTTGGCATATATACCTCAAC 1513  
QY 301 ACTATTATTAATGCAATCCTATATTTCTAGGTATAGAAGTTGATGATATACCTTTCTAC 360  
DB 1512 ACTATTATTAATGCAATCCTATATTTCTAGGTATAGAAGTTGATGATATACCTTTCTAC 1453  
QY 361 TTGCCATGCCATTACAAGACGCTGAGACTGAGCAACCACTGTGTTCATTCGATG 420  
DB 1452 TTGCCATGCCATTACAAGACGCTGAGACTGAGCAACCACTGTGTTCATTCGATG 1393  
QY 421 CAGGCTAGTAGTAAGTTGTTGCTGGTAGGAAAAAGGCTCTTATCTCACCTCCTTAA 480  
DB 1392 CAGGCTAGTAGTAAGTTGTTGCTGGTAGGAAAAAGGCTCTTATCTCACCTCCTTAA 1333  
QY 481 ACTAAAGGTTCTTCAGGCTTAATGTAAGGATGTCACCATCTCTTATCGAGGTTGCTT 540  
DB 1332 ACTAAAGGTTCTTCAGGCTTAATGTAAGGATGTCACCATCTCTTATCGAGGTTGCTT 1273  
QY 541 GAGCTGCAGATACATACATCGTTTCATGGTGATCCAACTGGATGCACTAGAGCCATG 600

DB 1272 GAGCTGCAGATACATACATCGTTTCATGGTATCCAACTGGATGTCAACTAGAGCCATG 1213  
QY 601 GTCCTTAGCTCTACCCCTCTCTTGTATGTGGCCAGGCTCAAACTGTAATACCT 652  
DB 1212 GTCCTTAGCTCTACCCCTCTCTTGTATGTGGCCAGGCTCAAACTGTAATACCT 1161

# RESULT 7

US-10-260-539-7/c

Sequence 7, Application US/10260539

Publication No. US20030073637A1

GENERAL INFORMATION:

APPLICANT: ERIKSSON, Ulf

APPLICANT: AASE, Karin

APPLICANT: LI, Xuri

APPLICANT: PONTEN, Annica

APPLICANT: UTELA, Marko

APPLICANT: ALITALO, Kari

APPLICANT: OESTMAN, Arne

APPLICANT: HELDIN, Carl-Henrik

TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES

FILE REFERENCE: 1064/44833C2

CURRENT APPLICATION NUMBER: US/10/260,539

CURRENT FILING DATE: 2002-10-01

PRIOR APPLICATION NUMBER: US/10/086,623

PRIOR FILING DATE: 2000-03-04

PRIOR APPLICATION NUMBER: US 60/107,852

PRIOR FILING DATE: 1998-11-10

PRIOR APPLICATION NUMBER: US 60/113,997

PRIOR FILING DATE: 1998-12-28

PRIOR APPLICATION NUMBER: US 60/150,604

PRIOR FILING DATE: 1999-08-26

PRIOR APPLICATION NUMBER: US 60/157,108

PRIOR FILING DATE: 1999-10-04

PRIOR APPLICATION NUMBER: US 60/157,756

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: US 09/438,046

PRIOR FILING DATE: 1999-11-10

PRIOR APPLICATION NUMBER: US 09/691,200

PRIOR FILING DATE: 2000-10-19

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PatentIn version 3.1

SEQ ID NO 7

LENGTH: 2253

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (176)..(1288)

OTHER INFORMATION:

US-10-260-539-7

Query Match

Best Local Similarity 2.0%; Score 601; DB 9; Length 2253;

Matches 651; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTATATGTAAGAACGCTCATCTTTTGATTTTAAATACAAAGATGCTTTCTTAAGAGA 60  
DB 1812 GTATATGTAAGAACGCTCATCTTTTGATTTTAAATACAAAGATGCTTTCTTAAGAGA 1753  
QY 61 GCAAGATTCAAAATGTTTGTGTTTCAAAATTTTAAATTAATTTATCTCTAAATTTT 120  
DB 1752 GCAAGATTCAAAATGTTTGTGTTTCAAAATTTTAAATTAATTTATCTCTAAATTTT 1693  
QY 121 CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAGAGATTTTAAGAGTCT 180  
DB 1692 CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAGAGATTTTAAGAGTCT 1633  
QY 181 AACTCAACATATGTAAGCTCTGGTGACCTGGTTATATATACCAAAAAAACATTTGAT 240  
DB 1632 AACTCAACATATGTAAGCTCTGGTGACCTGGTTATATATACCAAAAAAACATTTGAT 1573

```
QY 241 CTATATACACATAGACATGAATATATTTCTGTGTGTGTGTGTGCATATATAAACCCTCAAAAC 300
Db 1572 CTATATACACATAGACATGAATATATTTCTGTGTGTGTGTGTGCATATATAAACCCTCAAAAC 1513
QY 301 ACTATTATTAAGTAAAGCAATCCTATATCTTTAGGTATAGAAAGTTCATGATATACCTTTCTAC 360
Db 1512 ACTATTATTAAGTAAAGCAATCCTATATCTTTAGGTATAGAAAGTTCATGATATACCTTTCTAC 1453
QY 361 TTGCCATGGCATTAAACAAAGCAAGGCTGAGACTCAGCAACCACTTGTGTTCATTGCAATG 420
Db 1452 TTGCCATGGCATTAAACAAAGCAAGGCTGAGACTCAGCAACCACTTGTGTTCATTGCAATG 1393
QY 421 CAGGCTAGTAGTAAGTTTGGTGTGCTGTAGGAAAGGCTCTCTTATCTACCCCTCCCTTAA 480
Db 1392 CAGGCTAGTAGTAAGTTTGGTGTGCTGTAGGAAAGGCTCTCTTATCTACCCCTCCCTTAA 1333
QY 481 ACTAAAGGTTCTTTCAGGCTTAATGTAAGGATGTGCACATCTCTTATCGAGGTGTCCT 540
Db 1332 ACTAAAGGTTCTTTCAGGCTTAATGTAAGGATGTGCACATCTCTTATCGAGGTGTCCT 1273
QY 541 GAGCTGCAGATACAAATCGATCGTTCATGGTGATCCAACTGGATGCAACTAGAGCCATG 600
Db 1272 GAGCTGCAGATACAAATCGATCGTTCATGGTGATCCAACTGGATGCAACTAGAGCCATG 1213
QY 601 GTCTTAGCTACCCCTCTCTTTGATGTGGCCAGGCTCAAACTGTAATACCT 652
Db 1212 GTCTTAGCTACCCCTCTCTTTGATGTGGCCAGGCTCAAACTGTAATACCT 1161
```

RESULT 8

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US-09-915-582-17/c
; Sequence 17, Application US/09915582
; Patent No. US20020120103A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: PS723P1
; CURRENT APPLICATION NUMBER: US/09/915,582
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/231,968
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 3798
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-915-582-17
```

Query Match 2.0%; Score 601; DB 10; Length 3798;  
Best Local Similarity 99.8%; Pred. No. 2.le-262;  
Matches 651; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GTATATGTAAGAAGCCTCATCTTTTGATTTTAAATATAAAGATGCTTTCTTTAAAGAGA 1743
Db 1802 GTATATGTAAGAAGCCTCATCTTTTGATTTTAAATATAAAGATGCTTTCTTTAAAGAGA 1743
QY 61 GCAAGATTCAAAATGTTTGTCTTCAAAATTTAAATATATATCTCCCTAAATTTT 120
Db 1742 GCAAGATTCAAAATGTTTGTCTTCAAAATTTAAATATATATCTCCCTAAATTTT 1683
QY 121 CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAGGATTTTAAGAGTCT 180
Db 1682 CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAGGATTTTAAGAGTCT 1623
QY 181 AACTCAACATATGTAGCTCTGGTGTACCTGCTTATATATACCAAAAAAACAATTGAT 240
```

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Db 1622 AACTCAACATATGTAGCTCTGGTGTACCTGCTTATATATACCAAAAAAACAATTGAT 1563
QY 241 CTATATACACATAGACATGAATATATTTCTGTGTGTGTGTGTGCATATATAAACCCTCAAAAC 300
Db 1562 CTATATACACATAGACATGAATATATTTCTGTGTGTGTGTGTGCATATATAAACCCTCAAAAC 1503
QY 301 ACTATTATTAAGTAAAGCAATCCTATATCTTTAGGTATAGAAAGTTCATGATATACCTTTCTAC 360
Db 1502 ACTATTATTAAGTAAAGCAATCCTATATCTTTAGGTATAGAAAGTTCATGATATACCTTTCTAC 1443
QY 361 TTGCCATGGCATTAAACAAAGCAAGGCTGAGACTCAGCAACCACTTGTGTTCATTGCAATG 420
Db 1442 TTGCCATGGCATTAAACAAAGCAAGGCTGAGACTCAGCAACCACTTGTGTTCATTGCAATG 1383
QY 421 CAGGCTAGTAGTAAGTTTGGTGTGCTGTAGGAAAGGCTCTCTTATCTACCCCTCCCTTAA 480
Db 1382 CAGGCTAGTAGTAAGTTTGGTGTGCTGTAGGAAAGGCTCTCTTATCTACCCCTCCCTTAA 1323
QY 481 ACTAAAGGTTCTTTCAGGCTTAATGTAAGGATGTGCACATCTCTTATCGAGGTGTCCT 540
Db 1322 ACTAAAGGTTCTTTCAGGCTTAATGTAAGGATGTGCACATCTCTTATCGAGGTGTCCT 1263
QY 541 GAGCTGCAGATACAAATCGATCGTTCATGGTGATCCAACTGGATGCAACTAGAGCCATG 600
Db 1262 GAGCTGCAGATACAAATCGATCGTTCATGGTGATCCAACTGGATGCAACTAGAGCCATG 1203
QY 601 GTCTTAGCTACCCCTCTCTTTGATGTGGCCAGGCTCAAACTGTAATACCT 652
Db 1202 GTCTTAGCTACCCCTCTCTTTGATGTGGCCAGGCTCAAACTGTAATACCT 1151
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RESULT 9

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US-09-915-582-35/c
; Sequence 35, Application US/09915582
; Patent No. US20020120103A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: PS723P1
; CURRENT APPLICATION NUMBER: US/09/915,582
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/231,968
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 4001
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-915-582-35
```

Query Match 2.0%; Score 601; DB 10; Length 4001;  
Best Local Similarity 99.8%; Pred. No. 2.le-262;  
Matches 651; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GTATATGTAAGAAGCCTCATCTTTTGATTTTAAATATAAAGATGCTTTCTTTAAAGAGA 60
Db 1999 GTATATGTAAGAAGCCTCATCTTTTGATTTTAAATATAAAGATGCTTTCTTTAAAGAGA 1940
QY 61 GCAAGATTCAAAATGTTTGTCTTCAAAATTTAAATATATATCTCCCTAAATTTT 120
Db 1939 GCAAGATTCAAAATGTTTGTCTTCAAAATTTAAATATATATCTCCCTAAATTTT 1880
QY 121 CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAGGATTTTAAGAGTCT 180
Db 1879 CTAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAGGATTTTAAGAGTCT 1820
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QY 181 AACTCAACATATGTAAGCTCTGGTGACCTGGTTATATATACCAAAAAAACATTTGAT 240  
Db 1819 AACTCAACATATGTAAGCTCTGGTGACCTGGTTATATATACCAAAAAAACATTTGAT 1760  
QY 241 CTATATACACATAGACATGAATATATTTCTGTGTGTGTTTGTGCATATATACCTCAAAAC 300  
Db 1759 CTATATACACATAGACATGAATATATTTCTGTGTGTGTTTGTGCATATATACCTCAAAAC 1700  
QY 301 ACTATTATTAATGCAATCCTATATCTTTAGGTATAGAAAGTTGATGATATACCTTTCTAC 360  
Db 1699 ACTATTATTAATGCAATCCTATATCTTTAGGTATAGAAAGTTGATGATATACCTTTCTAC 1640  
QY 361 TTGCCATGCCATTAAACAAGCAAGGCTGAGACTCAGCAACCACTTGTGTTCATTGCATTG 420  
Db 1639 TTGCCATGCCATTAAACAAGCAAGGCTGAGACTCAGCAACCACTTGTGTTCATTGCATTG 1580  
QY 421 CAGGCTAGTAGTAAGTTTGGTTGCTGGTAGGAAAGGGTCTCTTATCTCACCTCCTTAA 480  
Db 1579 CAGGCTAGTAGTAAGTTTGGTTGCTGGTAGGAAAGGGTCTCTTATCTCACCTCCTTAA 1520  
QY 481 ACTAAAGGTTCTTTTCAGGCTTAATGTAAAGGATGTGCACATTTCTTTATCGAGGTGCTCTT 540  
Db 1519 ACTAAAGGTTCTTTTCAGGCTTAATGTAAAGGATGTGCACATTTCTTTATCGAGGTGCTCTT 1460  
QY 541 GAGCTGCAGATACAATCACATCGTTCATGGTGATCCCACTGGATGTCAACTAGAGCCATG 600  
Db 1459 GAGCTGCAGATACAATCACATCGTTCATGGTGATCCCACTGGATGTCAACTAGAGCCATG 1400  
QY 601 GTCTTAGCTCTACCCCTCTCTTTGATGTGGCCAGGCTCAAACTGTAATACCT 652  
Db 1399 GTCTTAGCTCTACCCCTCTCTTTGATGTGGCCAGGCTCAAACTGTAATACCT 1348

RESULT 10

US-09-915-582-37  
; Sequence 37, Application US/09915582  
; Patent No. US20020120103A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 17 Human Secreted Proteins  
; FILE REFERENCE: PS723P1  
; CURRENT APPLICATION NUMBER: US/09/915,582  
; CURRENT FILING DATE: 2001-07-27  
; PRIOR APPLICATION NUMBER: PCT/US01/01431  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/231,968  
; PRIOR FILING DATE: 2000-09-12  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 37  
; LENGTH: 2726  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-915-582-37

Query Match 1.7%; Score 499; DB 10; Length 2726;  
Best Local Similarity 99.5%; Pred. No. 5.3e-216;  
Matches 649; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTATATGTAAGAAAGCCCTCATCTTTTGTATTTTATATACAGATGCTTTCTTTAAGAGA 60  
Db 2002 GTATATGTAAGAAAGCCCTCATCTTTTGTATTTTATATACAGATGCTTTCTTTAAGAGA 2061  
QY 61 GCAAGATTCAAAATTTGTTTGTGTTTCAAAATTTTAAAAATTAATTTATCTCCTAAATTTT 120  
Db 2062 GCAAGATTCAAAATTTGTTTGTGTTTCAAAATTTTAAAAATTAATTTATCTCCTAAATTTT 2121  
QY 121 CTAAGACATGTTTTCATATATTTTGACCATCCCTTATTTTGCAAGGATTTTAAAGTCT 180

;

;

Db 2122 CTAAGACATGTTTCATATATTTTGACCATCCCTTATTTTGGCAAGGATTTTAAAGAGTCT 2181  
QY 181 AACTCAACATATGTAAGCTCTGGTGACCTGGTTATATATACCAAAAAAACATTTGAT 240  
Db 2182 AACTCAACATATGTAAGCTCTGGTGACCTGGTTATATATACCAAAAAAACATTTGAT 2241  
QY 241 CTATATACACATAGACATGAATATATTTCTGTGTGTGTTTGTGCATATATACCTCAAAAC 300  
Db 2242 CTATATACACATAGACATGAATATATTTCTGTGTGTGTTTGTGCATATATACCTCAAAAC 2301  
QY 301 ACTATTATTAATGCAATCCTATATCTTTAGGTATAGAAAGTTGATGATATACCTTTCTAC 360  
Db 2302 ACTATTATTAATGCAATCCTATATCTTTAGGTATAGAAAGTTGATGATATACCTTTCTAC 2361  
QY 361 TTGCCATGCCATTAAACAAGCAAGGCTGAGACTCAGCAACCACTTGTGTTCATTGCATTG 420  
Db 2362 TTGCCATGCCATTAAACAAGCAAGGCTGAGACTCAGCAACCACTTGTGTTCATTGCATTG 2421  
QY 421 CAGGCTAGTAGTAAGTTTGGTTGCTGGTAGGAAAGGGTCTCTTATCTCACCTCCTTAA 480  
Db 2422 CAGGCTAGTAGTAAGTTTGGTTGCTGGTAGGAAAGGGTCTCTTATCTCACCTCCTTAA 2481  
QY 481 ACTAAAGGTTCTTTTCAGGCTTAATGTAAAGGATGTGCACATTTCTTTATCGAGGTGCTCTT 540  
Db 2482 ACTAAAGGTTCTTTTCAGGCTTAATGTAAAGGATGTGCACATTTCTTTATCGAGGTGCTCTT 2541  
QY 541 GAGCTGCAGATACAATCACATCGTTCATGGTGATCCCACTGGATGTCAACTAGAGCCATG 600  
Db 2542 GAGCTGCAGATACAATCACATCGTTCATGGTGATCCCACTGGATGTCAACTAGAGCCATG 2601  
QY 601 GTCTTAGCTCTACCCCTCTCTTTGATGTGGCCAGGCTCAAACTGTAATACCT 652  
Db 2602 GTCTTAGCTCTACCCCTCTCTTTGATGTGGCCAGGCTCAAACTGTAATACCT 2653

RESULT 11

US-09-954-531-902  
; Sequence 902, Application US/09954531  
; Patent No. US20020165180A1  
; GENERAL INFORMATION:  
; APPLICANT: Weaver, Zoe  
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C  
; FILE REFERENCE: Gene Sets  
; CURRENT APPLICATION NUMBER: US/09/954,531  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: US/60/233,133  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US/60/234,009  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,034  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,509  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: US/60/234,567  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 1392  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 902  
; LENGTH: 485  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-954-531-902

Query Match 1.5%; Score 460; DB 9; Length 485;  
Best Local Similarity 100.0%; Pred. No. 2.6e-198;  
Matches 460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATATGTAAGAAAGCCCTCATCTTTTGTATTTTATATACAGATGCTTTCTTTAAGAGA 60  
Db 26 GTATATGTAAGAAAGCCCTCATCTTTTGTATTTTATATACAGATGCTTTCTTTAAGAGA 85  
QY 61 GCAAGATTCAAAATTTGTTTGTGTTTCAAAATTTTAAAAATTAATTTATCTCCTAAATTTT 120



Db	86	GC	AAGATTC	CAAAATGTTT	TGTGTTCCAA	AAATTTAA	AAATTAAT	TATCCT	TAATTTT	145
QY	121	CT	AAGACAT	GTTTTC	ATATATTT	GACCAT	CCCTTATTT	TGGC	AAAGATTTT	180
Db	146	CT	AAGACAT	GTTTTC	ATATATTT	GACCAT	CCCTTATTT	TGGC	AAAGATTTT	205
QY	181	AA	CTCAAC	ATATG	TAGC	TC	TG	GTG	TACCTGGT	240
Db	206	AA	CTCAAC	ATATG	TAGC	TC	TG	GTG	TACCTGGT	265
QY	241	CT	ATATAC	ACATAG	ACATGA	ATATAT	TTCTGT	GTGTTGT	GCATATATA	300
Db	266	CT	ATATAC	ACATAG	ACATGA	ATATAT	TTCTGT	GTGTTGT	GCATATATA	325
QY	301	AC	TATATTA	AAATGC	CAATCCT	ATATCTT	TAGGTAT	AGAA	GTGATATAC	360
Db	326	AC	TATATTA	AAATGC	CAATCCT	ATATCTT	TAGGTAT	AGAA	GTGATATAC	385
QY	361	TT	GCCAT	TGGCAT	TAA	CAAAAG	CAAGGCT	TG	GAC	420
Db	386	TT	GCCAT	TGGCAT	TAA	CAAAAG	CAAGGCT	TG	GAC	445
QY	421	CAG	CTAG	TAGT	AA	GGTTT	TGGTTG	CT	TGAG	460
Db	446	CAG	CTAG	TAGT	AA	GGTTT	TGGTTG	CT	TGAG	485

✓ **RESULT 12**

US-10-139-583-36/c ; Sequence 36, Application US/10139583  
; Patent No. US20020177193A1

```

; PATENT NO: 052002017/193A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
;
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
;
; FILE REFERENCE: 98-60
;
; CURRENT APPLICATION NUMBER: US/10/139,583
; CURRENT FILING DATE: 2002-05-02
;
; PRIOR APPLICATION NUMBER: 09/457,066
; PRIOR FILING DATE: 1999-12-07
;
; NUMBER OF SEQ ID NOS: 50
;
; SOFTWARE: FastSeq for Windows Version 3.0
;
; SEQ ID NO 36
;

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	Query Match	Best Local Similarity	1.3%;	Score 377;	DB 9;	Length 1882;			
	Matches 427;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	225	AAAAAAACATTGATCTATATACATACACATGATATATATTTCTGTGTGTTTGTGTC	284						
Db	1638	AAAAAAACATTTGATCTATATACATACACATGAATATATTTCTGTGTGTTTGTGTC	1579						
QY	285	ATATATAACCTCAAAACACTATTATTAATGCAATCCTATATTTCTTAGGTATAGAAAGTTGA	344						
Db	1578	ATATATAACCTCAAAACACTATTATTAATGCAATCCTATATTTCTTAGGTATAGAAAGTTGA	1519						
QY	345	TGATATACCTTTCTACTTGGCCATGGGCAATTAACAAAGCAAGCGTGAGACTCAGCAACCACT	404						
Db	1518	TGATATACCTTTCTACTTGGCCATGGGCAATTAACAAAGCAAGCGTGAGACTCAGCAACCACT	1459						

Qy	405	TGTGTTTCATGCGATTCGAGGCTAGTAGTAGTTTGGTTGCTGCTAGGAAAGGCTCTCTT	464
Db	1458	TGTGTTTCATGCGATTCGAGGCTAGTAGTAGTTTGGTTGCTGCTAGGAAAGGCTCTCTT	1399
Qy	465	ATCTCACCCCTCCCTTAAACTAAAGGTCCTTTTCAGGCTTAATGTAAAGATGTGCACATTCCTC	524
Db	1398	ATCTCACCCCTCCCTTAAACTAAAGGTCCTTTTCAGGCTTAATGTAAAGATGTGCACATTCCTC	1339
Qy	525	TTATFCGAGGTGGTCCTTGAGCTGCAGATACAAATCACATCGTTCATGCTGATGCCAACCTGGAT	584
Db	1338	TTATFCGAGGTGGTCCTTGAGCTGCAGATACAAATCGCATCGTTCATGCTGATGCCAACCTGGAT	1279
Qy	585	GTAACCTAGAGCCATGGTCTTAGCTCTACCCCTCCTCTTGATGTGGCCAGGCTCAAACCTG	644
Db	1278	GTCACCTAGAGCCATGGTCTTAGCTCTACCCCTCCTCTTGATGTGGCCAGGCTCAAACCTG	1219
Qy	645	TAATACCT	652
Db	1218	TAATACCT	1211

RESULT 13

```

RESOLV 13
US-10-039-847A-1/c
: Sequence 1, Application US/10039847A
: Publication No. US20020183273A1
: GENERAL INFORMATION:
: APPLICANT: Hart, Charles E.
: APPLICANT: TOPOUZIS, Stavros
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING
: TITLE OF INVENTION: KIDNEY FUNCTION
: FILE REFERENCE: 00-100
: CURRENT APPLICATION NUMBER: US/10/039,847A
: CURRENT FILING DATE: 2002-06-17
: PRIOR APPLICATION NUMBER: US 60/244,479
: PRIOR FILING DATE: 2000-10-30
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 1
: LENGTH: 1882
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (226)...(1338)
US-10-039-847A-1

```

	Query Match	1.3%	Score 377;	DB 9;	Length 1882;
	Best Local Similarity 99.8%;	Pred; No. 1.7e-160;			
	Matches 427; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	225	AAAAAAAAACATTTGCATCTATATACACATACACATGAAATATATTTCTGCTGCTGCTTTGCTGC	284		
Db	1638	AAAAAAAAACATTTGATCTATATACACATACACATGAAATATATTTCTGCTGCTGCTTTGCTGC	1579		
Qy	285	ATATATAACCTCAAAACACTATTATTAATGCAATCCTATATTTCTTAGGTATAGAAGTTGA	344		
Db	1578	ATATATAACCTCAAAACACTATTATTAATGCAATCCTATATTTCTTAGGTATAGAAGTTGA	1519		
Qy	345	TGATATACCTTTTCTACCTGGCATTTAAACAAAGCAGGCTGAGACTCAGCAACCACT	404		
Db	1518	TGATATACCTTTTCTACTTGGCATGGCATTTAAACAAAGCAGGCTGAGACTCAGCAACCACT	1459		
Qy	405	TGCTTTCATTTGCATTGCGAGCTAGTAGTAGTTTGGTTGCTGCTAGGAAAGGCTCTCTT	464		
Db	1458	TGCTTTCATTTGCATTGCGAGCTAGTAGTAGTTTGGTTGCTGCTAGGAAAGGCTCTCTT	1399		
Qy	465	ATCTCACCCCTCCCTTAAACTTCTTTTCAGGCTTAATGTAAAGATGTGCACATTCTC	524		
Db	1398	ATCTCACCCCTCCCTTAARACTAAAGGTTCTTTTCAGGCTTAATGTAAAGATGTGCACATTCTC	1339		
Qy	525	TTATCGAGGTGGTCTTGAGCTGCAGATACAAATCACATCGTTTCATGTGTGATCCAACTGGAT	584		
Db	1338	TTATCGAGGTGGTCTTCAGCTGCAGATACAAATCGCATCGTTTCATGTGTGATCCAACTGGAT	1279		

QY 585 GTCAACTAGAGCCATGGTCTTAGCTCTACCCCTCTCTTGTATGTGCCAGGCTCAAACTG 644  
|||||  
Db 1278 GTCAACTAGAGCCATGGTCTTAGCTCTACCCCTCTCTTGTATGTGCCAGGCTCAAACTG 1219  
|||||  
QY 645 TAATACCT 652  
|||||  
Db 1218 TAATACCT 1211

## RESULT 14

US-10-226-559-1/c  
; Sequence 1, Application US/10226559  
; Publication No. US20030105015A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilbertson, Debra G.  
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
; FILE REFERENCE: 00-28  
; CURRENT APPLICATION NUMBER: US/10/226,559  
; PRIOR FILING DATE: 2002-08-23  
; PRIOR APPLICATION NUMBER: US/09/540,224  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: US 60/180,169  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1882  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (226)...(1338)  
US-10-226-559-1

Query Match 1.3%; Score 377; DB 9; Length 1882;

Best Local Similarity 99.8%; Pred. No. 1.7e-160;

Matches 427; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 225 AAAAAAATTTGATCTATATACACATAGACATGAATATATTTCTGTGTGTTGTGC 284  
|||||  
Db 1638 AAAAAAATTTGATCTATATACACATAGACATGAATATATTTCTGTGTGTTGTGC 1579  
|||||  
QY 285 ATATATAACCTCAAAACACTATTATTAATGCAATCCTATATTTCTTAGGTATAGAAGTTGA 344  
|||||  
Db 1578 ATATATAACCTCAAAACACTATTATTAATGCAATCCTATATTTCTTAGGTATAGAAGTTGA 1519  
|||||  
QY 345 TGATATACCTTTCTACTTGGCATTTAACAAGCAAGGCTGAGACTCAGCAACCACT 404  
|||||  
Db 1518 TGATATACCTTTCTACTTGGCATTTAACAAGCAAGGCTGAGACTCAGCAACCACT 1459  
|||||  
QY 405 TGTGTTTCATTCATTCAGGCTAGTAGTAAGTTTGGTTGCTGGTAGGAAAAGGTTCTCTT 464  
|||||  
Db 1458 TGTGTTTCATTCATTCAGGCTAGTAGTAAGTTTGGTTGCTGGTAGGAAAAGGTTCTCTT 1399  
|||||  
QY 465 ATCTCACCTCCCTTAAACTTAAAGGTTCTTTTCAGGCTTAATGTAAGGATGTGCACATCTTC 524  
|||||  
Db 1398 ATCTCACCTCCCTTAAACTTAAAGGTTCTTTTCAGGCTTAATGTAAGGATGTGCACATCTTC 1339  
|||||  
QY 525 TTATCGAGTGGTCTTAGCTGCAGATACAATCAGATCGTTTCATGGTATCCAACTGGAT 584  
|||||  
Db 1338 TTATCGAGTGGTCTTAGCTGCAGATACAATCAGATCGTTTCATGGTATCCAACTGGAT 1279  
|||||  
QY 585 GTCAACTAGAGCCATGGTCTTAGCTCTACCCCTCTCTTGTATGTGCCAGGCTCAAACTG 644  
|||||  
Db 1278 GTCAACTAGAGCCATGGTCTTAGCTCTACCCCTCTCTTGTATGTGCCAGGCTCAAACTG 1219  
|||||  
QY 645 TAATACCT 652  
|||||  
Db 1218 TAATACCT 1211

RESULT 15  
US-10-274-638-1/c  
; Sequence 1, Application US/10274638  
; Publication No. US20030109000A1  
; GENERAL INFORMATION:  
; APPLICANT: Moore, Margaret D.  
; APPLICANT: Fox, Brian A.  
; TITLE OF INVENTION: DIMERIZED GROWTH FACTOR AND MATERIALS  
; FILE REFERENCE: 01-30  
; CURRENT APPLICATION NUMBER: US/10/274,638  
; CURRENT FILING DATE: 2002-10-18  
; PRIOR APPLICATION NUMBER: 60/346,117  
; PRIOR FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1882  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (226)...(1338)  
US-10-274-638-1

Query Match 1.3%; Score 377; DB 9; Length 1882;

Best Local Similarity 99.8%; Pred. No. 1.7e-160;

Matches 427; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 225 AAAAAAATTTGATCTATATACACATAGACATGAATATATTTCTGTGTGTTGTGC 284  
|||||  
Db 1638 AAAAAAATTTGATCTATATACACATAGACATGAATATATTTCTGTGTGTTGTGC 1579  
|||||  
QY 285 ATATATAACCTCAAAACACTATTATTAATGCAATCCTATATTTCTTAGGTATAGAAGTTGA 344  
|||||  
Db 1578 ATATATAACCTCAAAACACTATTATTAATGCAATCCTATATTTCTTAGGTATAGAAGTTGA 1519  
|||||  
QY 345 TGATATACCTTTCTACTTGGCATTTAACAAGCAAGGCTGAGACTCAGCAACCACT 404  
|||||  
Db 1518 TGATATACCTTTCTACTTGGCATTTAACAAGCAAGGCTGAGACTCAGCAACCACT 1459  
|||||  
QY 405 TGTGTTTCATTCATTCAGGCTAGTAGTAAGTTTGGTTGCTGGTAGGAAAAGGTTCTCTT 464  
|||||  
Db 1458 TGTGTTTCATTCATTCAGGCTAGTAGTAAGTTTGGTTGCTGGTAGGAAAAGGTTCTCTT 1399  
|||||  
QY 465 ATCTCACCTCCCTTAAACTTAAAGGTTCTTTTCAGGCTTAATGTAAGGATGTGCACATCTTC 524  
|||||  
Db 1398 ATCTCACCTCCCTTAAACTTAAAGGTTCTTTTCAGGCTTAATGTAAGGATGTGCACATCTTC 1339  
|||||  
QY 525 TTATCGAGTGGTCTTAGCTGCAGATACAATCAGATCGTTTCATGGTATCCAACTGGAT 584  
|||||  
Db 1338 TTATCGAGTGGTCTTAGCTGCAGATACAATCAGATCGTTTCATGGTATCCAACTGGAT 1279  
|||||  
QY 585 GTCAACTAGAGCCATGGTCTTAGCTCTACCCCTCTCTTGTATGTGCCAGGCTCAAACTG 644  
|||||  
Db 1278 GTCAACTAGAGCCATGGTCTTAGCTCTACCCCTCTCTTGTATGTGCCAGGCTCAAACTG 1219  
|||||  
QY 645 TAATACCT 652  
|||||  
Db 1218 TAATACCT 1211

Search completed: July 8, 2003, 19:41:40

Job time : 3100 secs